

(D) Fig. 2a-h (i) 116 97 ≥ ш 45 97 9 V8-protease elastase (a) (a)

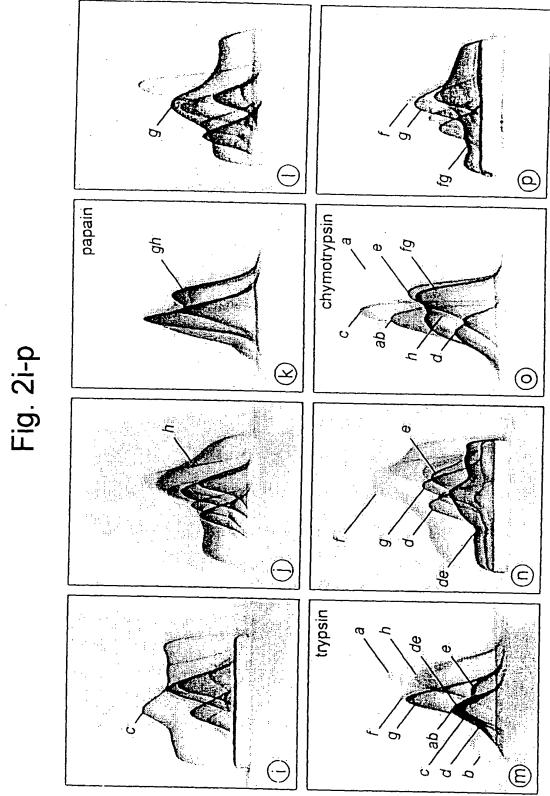
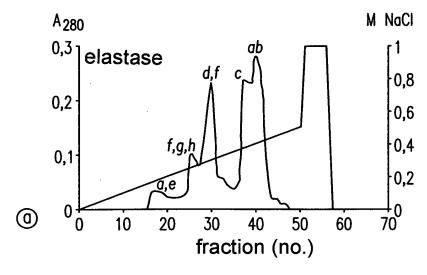
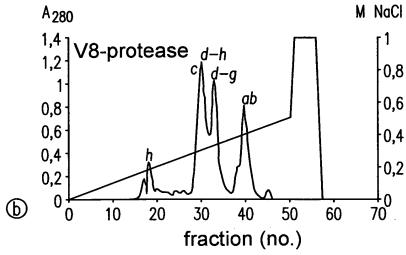
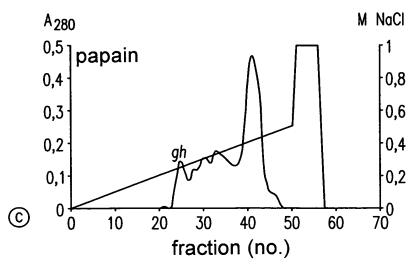


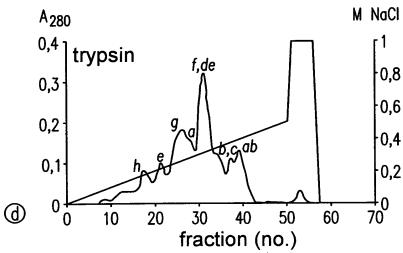
Fig. 3a-c

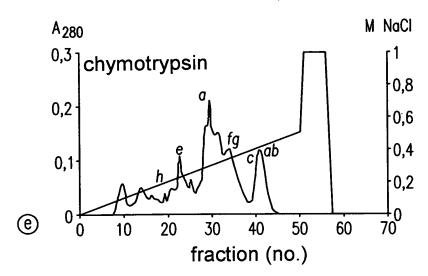












# Figure 4

# Genomic sequence of the HtH1 gene

SIGNAL PEPTIDE SEQUENCE 1S-1 (1st part)

GGCTTGTTCAGTTTCTACTCGTCGCCCTTGTG

INTRON 1S-1/1S-2 (SEQ ID NO:109)

TTACAACCAACGTGTCTCTATTGGTCTTCACCTGTTTAACGTATATATTGTTTTTAATGT GAAAATCTGAGATTATTTTCATTTCCGTCAATATTCGTAAAATACTATACAAATAAAATT GCTTCAGCCTATTGCATTGGCAGTTTTCGCAGAATAACGAGGGAAGGCGTACATAAAATA TAAACCAGTGTATATTCAAGCATGTTTATAATTTCTTTATAGATTATAACATCATATCAA AACACCAATCTGGATTTAAACCCGTGAATCCAAAGTATACCAATTAACGGAACTTTATCA TGTTTTATCAAAGGTTTTAGATGAGGGTAAAGAAGTCCGAGCTATATTTTGCGATATCAG CAAAGCCTTCTATCACGTCTTGCACACAGGGCTGGTATCTAAACTCGAATCCACAGGAAT AAATATTTCAGCCGATAGAGAACAGTCGGTGGCTATCATTGGTCACAAAACAAGTCCAAA ATCTGCATTAGCCGGTGTTCCCCAAGGCTCTGTCTTGGGGCCACTATTATTTCTCACCTA TATAAACGATTCAACTAATGGAATATAAAGCAACGTAAACCTCACCGCAGATGAAACACT AAGTTATAGACAATCCGTTTAAAACCCAGCCACTGCTTAATAATGACTTAGGCCGTCTTT CAGACTGGGCTAGTAAGCGGCAGGTTAAATTTCACCTTGAAAAGACAGAAACCATGGTAT ATTTCAAAAACACGAATGCAAGTCCTAAACTTCAACTACTTGATGATACTGGGATTT TGTTTTTTTCAATAACACGAATGCAAGTCCTAAACTTCAACTACTTGATGATACTG GGATTTCTAAAGTGTGTGGTGAACACAAACACCTTGGCCTGATTCTGCAAGATAATGGAA AATGTCAGAAACATAAGCAAGTTGATGTGGGGGTTTTCTGGGGGGTTGTGACAACACCGAAA GACCCTGCAACTAATGTTAGCTCAAAGGGTTTTACACCCGGTCACAAGTGGGGATCGACC CAGGCACCTTTTGCCTTTGACAGCTCGCCTTTCAAAAAAATCTCAAATTCGAAAACGAAATC TAATAATTTCATGAGCGATACAACCGTTTTTCATAATGCTGTGGTACCGCATACTGTGGA AACATCTGTCTACCCATTTGGTAGTCCCCCATAAAATGTATTTATGTTTATAAACACAAT GTTTATAGGGTTACAGTTAGAAGAAGCATTTCTATTGGCTAATGTACATTGCTTGTTTTT ACTATTGTGCAAAGGCATATTACAGGTCTTTTAGGAAATTAAATACTGTTTAAATCACAT ACACTACCGGTAATCCTATTATGCTTATCCTGCCAACATTCTGCCCAAGCAAACGCATGA AAGTTAAAGCTGAGTGTAAAATACTGATTGCTGTGTTACTTCACAACCAGTGGACTGAAT ACAACCATGTTTTTCTTGAAAGTCACAAACATCCAGTCGGTTTCTAATGTGTTAAGTTT GACTCCTAGTTCGTTACTTTTTTAATAAAACATCCATGTGTTTAATGTTTTGGCCACAGAT ATAACAAGAAAGAAATCGGATAAAATCTACATTTTGACCAATCGGAAGGCTGCCCCCTCC CTAATCCTAATCATTTTTGTGCCTCAAAACATACTCAACCAGACATTTGAACTATGTATA TGCACAGACATGTGGTTGAGACACACTTGATTCAGTGCAGGATTATGTCCTTCAACCGAG TGTAGTCTTTAAGTGTGCCTGGAAACAAAAACTGCGTTGGGTTGCATCGCCTCTGTAGC AAGCTTGGACGCGTCACGCAGCTCTGATACCACGTATTGGCACCATGTTTCATCGGTCTC ACGCGAATATTATGCTATGTGTGGCGTATCATACCATAGGTTGGGAACGTTTCAATACTG TACCGAGCTTGGGCGTGTCACAAAGCTATGATAAGATGACAACACGTCTTGGCATCTTGT TTCCTCGGTATCACGCGCTGTTATGCTATGTGTGGCTATCACACCTTAGGTTGGGAAAGT

TTCCACATTTTCCAGCCTCGTACATGTTTCCTTTTGTTTTTTCCTTAGTTATCAGCATAC CGTATATTCTATATTTAATGAGCATTTGTATTTTTCTACAG

SIGNAL PEPTIDE SEQUENCE 1S-2(2nd part)

GTGGGGGCTGGAGCAG

INTRON 1S-2/1A-1 (SEQ ID NO:110)

GTGAGTTTCTTAACATTGTCATGGTACATGGATATACGCTCAGTGGGAAAGCAGGATATC CCCTTGGTTCAAGTATTCACTTGTCACGCCAAGTGTTCGATTCCCAACATGGAATACTGT CATATAGTAAATTGATACACTACTTACATTTAATTCTCCACTAAACGTCAACGTCCTTTA TAATGCTTATAAATATAAATTATATAAATACCTATAACTATAAATTAGTTATACTAGTAT TTATCAAAACATATTTGCCACGACACTGCACGCCGATACTTCAAGTGTCTTCACCTCAAG GCTTCATTAGTTTCGTCAGATGCGTGTATCCATACGAGTACATTCAGATTATGGGATCCA GAGACAGATGGCAACCGTTCTTTCCTCCTGACTAGGTGAGTGCCACTGATAAATCATTAT GCCTTTAACATTAGGAATGTTAGCAGTGCACATGTTTCAGAATTGCGACCTTATGGTTGT AAAGATTACAAACTTTACAACTTACTTGAGACAGGTTCCATATGTCGTATCTGAAATAGT GTGAAGGTATCTGATTCGATGCAATACACAGACATATAAACATATTGTCGCCCTGCTATT CCGGAAAGGTCATTTTGTATGTAACGTTCCTTAATGGACACAAACGGAATTATTAGTTAA ACATACTCAACAAAACTATGTTATTTTGCAATGGGTAGCACCGAAATCTACCGACAGTGG TTCGTAAAAGTAGAACATTCTGACATAAAGAAAAATCATTGGCTTTAAATATATGCAAGT TACTTGTCTCTAACAACCAGTTTTATACACATTTCAGAGAACGGGGAATCCGCGATGACA ATATCAACGAGTATATACAGAATATATAATTAAAAACGATGAGTGCCTGGCAAGGGAAAG AGCGAGATTTGCCAAACAGGGGGGTGGTGTTGAGCTTGAATCGTGGAGAAACGTAGATTG AAAGACAAGATGACATCTAATGATCCGAAAATCAAACACAGGATTAACTGGGATGCAGAA GAATGAATATCTCAAGCATACATGCAACACTTCATGAATGCATCTCAAACATTTTCGTCA GATCGGATGCATGAAGATTTGTAAAGCAATGGTTTAAATTGTCCCTAAACGTTTAGTTGG AGATGTATGAGGCTAGGCTGTATGTTGAACGAAACCATTTAACATTGTTGTTCATGATTA TTTAATATTTTTCATTTTATAGATGTACAATAAAATTGGAAACTAAACATTTCCCTTTA TTGTTTTGTATTTACCTGTTCATGGGTATGTTTTGAAAGATCGTGATATTTAGTTGGCAT TCACAAGTTGGAAAAAGGTCACTCAGTTTGATTTCAAGTTTATGTAACCTCTTTATCTGA CGCTCCAAAATATGTATAGCCTTGTTCATCTGTCGGTATGTGGATATTCCTACTTCAGGG TAGGGTAGCATTAATACTTACAAAACATAACGTGTACCAGATTTCAGTCACCTCAGAGAT ACCCTGAATCGGAATGATACGTTACACTTTAGAAACAATTCACAAATATGACTGTCACCC TTTCAGGTAATAATGTTTGACGGACTACGATAGTGCTGAACAGCAGGAGAGGCAACATGG TTCGATTGTGAGACAGGTTTAGTGTATTTGTTTGCGAATTTAAGGTTCTGAATCACAATA GCTGGGATAAAGCTTAGTGGGACGTTAAGTCCCATCTCAATCTCTCATTTTTTCCAAA ACAGTTTTAATTCAGGCTCATGACAAGGTCGTACTGTTGCAAAGGATTCTACTTCAAGCA GAGATGTCTCATGAATACAGTACAGGGTTTTTTGAAGTTTATCCAGTGCAGCGCTGGCACC ATCTCTGCATGCGAATTATACCATCCATGCCGCTCTAGGCTATTTGTATTAAGTCTGTAG AATTAAATTCGCGAGTTGCAAATACTGCTCACCATTATCTGCCTCAACCCAGTTTGGGTA CATGCGATTTACACAATATTATGTATAATGTTCGCTTTTCGAAAACAAAACACCTAAATT CATCCAAAGTTTTGGGAGATTTTATTCGAGAAATCAACCTGAGATGTTGAATCGGGAGCT GCGCTTATTCAATGGTGGACTCGGAAGGGAAGTAACCGCTGATGAGGCAAAACAATAACG TAATTTGACCATTCGAACAACTTTACTATTCTATTCATAATGTGTTTTAGATTTACATTTG AATTAAAAGAGATGAGTTTAAGATATTAATATTTTCCTTTTATAGTCTGTCGTGATTGTA

GGGCAATATTTATGTATGTTCGTTCATTTTTCATTTATCATTTGGAAAGGTATATCATAA TTCAATTTATTATCATCCGTCATCCAATTTTATTTCACGAAAGTATAAGAAATAACGAGA GAGAGAGAGAGAGAGAAAAGACAGAAATGAAGTTAGGAGATATNAGTTATCAAGAA AACAACAGTTTGAATTTTTTGTTTAGACAAGATATCATATCAATAACCTCGCACTATTAC GGGAATAGGCGGGCGTTCCATATGCACAATGAATCGTCAGTTAAAATCAACATTAAACTT AAAATACTCCTCATATTTAAAGTTGATCTACCTCTTGTATTATTGTAGACTATTAGACAG AAGTCGACAGTGACACCAGCAACCAGATATCATACCCAGACTTAAAAAGCTGTTTCCTTG ATGTTTCAATTTATTTCCATTTCCATTATTTCCCTTTATTGGTTTCCATTTATCAAACTT ATCAAGAATGTATAGGAGCTATTCCTTGTTCCTAAAACCGGATAGATCCATAATTTCCAT TTTGGGATAAATGGAAACTAAACACAACTTTTACAGTAAACACGAGTGAGCAAGTTGAGT TTTACGCCGTTTTTAGTAGTATTCCAGCAATATCGCGGCGGGGGACACCAGAAATGGGCT TCACACAGTGAATGCATGTGGGGATTCGAACCCGGGTCTTCGGCGTGACGAGTGAACGCT TTAGCCACTAGGCTACCCCACCGCCTATTTATAGTTAAGACGAATACTTTTCTCAAGCCT CAAATATGTCCATTCTAGAGAGACTGAATCTGATCCTGAATCTGCGGACCGGTCTTGAAT ATCATCCCACTAACTCATTGTACAAAGTACCTGTAGATTGTCAGTTCAAAGACAGATTTC TGATTTTAATCCTACTTTGAGATGTTTTAACTTTTATTCGATGCATTTTTTGCGTTCTGCG CGATCAGATTGAAACCGGAATGCACAGTGAAGTGTGGCATACATCTTTCCACAGAGATAC TGGATACTAGGTGGTACAACCGCATTGGCTTTGTGAAAGGATATTAGTGTTTTATGAGAC TGACTCATGTTTCAATGCTTAGAGCGGAATGATCTCGGTCTTCATGAAAAATATTGTGTT GAAGTAACCCCCAGTCCCTAACAGAACGTGGGGAAAGCAGATGGATATGCCAAGACATC TTCGCATGGTGTGAAGATGATCGTTACAACATCTGCAGAAAAAGTTATTTCTGTGAAGAA TATGCCAAAGCATCACTGTGAGTGTTTTGAAGATGTGATATGGCAACACGCAGCGTGTAA TTATGCTTTGTGTGTATTTCTGAAGATCCGTATGAGCATGGCGCCCAAACTATCAGTTAAA TGGCTATGCGAAGATCTTCCCGAGATGGTAAACACATATTTTGGCCATTTTCTTTGTAAG TGGGCGACACAGAAGATCCCCCTGATTGTGTGGATGAGGACACAAAAACGGGTCCCCCTT CCACCAACCACAGTTGTATAAATCGCTTGCGGACTTGAATACGGCAGTTGGACAGATAC ATACAGCCAGAGAGGGCCGAACTAAAACATCTAAACATGGAAAAACTGTAAAGACAGGCT TTGTTGTACGACGTACGTAAATTCATTGAATGTTTGAAAAGGTAGAAAATTATTAAATCT TTGAAACCTCGCTCTGTTTGTTTGTTATTGTCCCCCACATTTGCAAATGGTATCCAAAAA GGGCAGACACATTTGTTTTAATCTTAGCCAGGTTCAATTTAGCCTTGCGCCCAGACTCAT TGTATCTGGTGAAGGCTATAGGTGGCCACGTCTTCTAAGATGCTATGCTATTCTTACCAG TCTCTCCTACCCAGAGTTCACCTGCACTGCTCCTGACTCACAATAAGCTGACGTGCTGTC ATATATGTGCAACATTGTATACGTTGGCGTTAAGCCCAACTCACTTCCGCTGTCTTTTGG CAG

DOMAIN 1A-1 (1st part of domain a)

ACAACGTCGTCAGAAAGGACGTGAGTCACCTCACAGTTGACGAGGTGCAAGCTCTTCACG GCGCCCTCCATGACGTCACTGCATCTACAGGGCCTCTGAGTTTCGAAGACATAACATCTT ACCATGCCGCACCAGCGTCGTGTGACTACAAGGGACGGAAGATCGCCTGCTGTGTCCACG GTATGCCCAGTTTCCCCTTCTGGCACAGGGCATATGTCGTCCAAGCCGAGCGGGCACTGT TGTCCAAACGGAAGACTGTCGGAATGCCTTACTGGGACTGGACGCAAACGCTGACTCACT TACCATCTCTTGTGACTGAACCCATCTACATTGACAGTAAAGGTGGAAAG

INTRON 1A-1/1A-2 (SEQ ID NO:111)

GTAACTACAAACGTCGTCCCATTCATACAGGAGAAATATACAATTGTGTTGTAAGAGCGG TATACTGTTTGCCAACTGTGTAATTGAAACGTTGATGATGGTGTCTTTGTATTTCAATTT

### 10 / 44

GTATGCACTTAGACATGATCAATGTTTCTGATGTGTCAAGGATGTTCGGTGTCACTTT CAAAAGATCAAATTCATATGACGTACACAGAGCAAGAACCAACAGTAAGAAGTCTGTATG ACTTCGCTCTTAAAAGCAATGGAAAAATATTTTCACTTAACACCTAGCCCATAATCACGC ATATTAGATTATTCAAGCGATGTCAACATGTTTTTAATATCAATCTCATGGTTCTGATAT TACCGGAGACATGCAACAGGCTGCCATTATAGCCAGGAAATCTTATGAATATGTGCATAT TTTTTCTTTGATTCTGTATGACGAGAAATATTCGGAGGCAAAGATTGTGTTTTCAGAACA GAATCAGGGTATCAGTGACATCGTCACTGCATGGCTACAATATTGCTGATGTGACTGTTT CTCCAAGGATTTTCATCTCACTGTCTGTACTTTGAATCTACAAATTCGTATTAAAGTTAT GACAATTTTACCCCTGCCTATTTGTAAACGAAATATAACATGAGTGTTTTATGCTGACAG

DOMAIN 1A-2 (2nd part of domain a)

GCTCAAACCAACTACTGGTACCGCGGCGAGATAGCGTTCATCAATAAGAAGACTGCGCGA GCTGTAGATGATCGCCTATTCGAGAAGGTGGAGCCTGGTCACTACACACATCTTATGGAG ACTGTCCTCGACGCTCTCGAACAGGACGAATTCTGTAAATTTGAAATCCAGTTCGAGTTG GCTCATAATGCTATCCATTACTTGGTTGGCGGTAAATTTGA

INTRON 1A-2/1A-3 (SEQ ID NO:112)

GTAAGTTTGGTTTACAGTTTCATTATAAAAACATAGCAGTTTTAAGTTTAGGGGCAGATT CTAATCTCTAATATTCCTTTCAACTCACTTTATTGGTGCCTTCTTGGAGTGACATTTAGA AACTAAGACAAGAGGAAGATGAACAATGTTTGTAGGGATAGACAGCTTGGATGCAATTTC GGACCAGATTCTAACAGCGTCATGAAGCAAGTGATACACAACGTTATCAATAACGAGAAT ATACACATAGATGGTTTGAGTTTATAAATGAACTATTAACGGCATTGTGGTTATAGACAG TGAGGAAGACGCCAGATAGACAAAGGGTAGGGGCCTTGGTTAGATAATGAGAAGTTGAAG AGGTGTAATAACTTAAATCTCTCTTGACTATTGATTGTGTCTAAGAGTTTTCTTATCTTA CAGTCGGCCAGTTGGGTCAAAGATGTGTGTGTTCTGCGATG GCTGATTTAGAGTCAGTTTACTTCAGATGAATGAAGTTCCCCGATTCTTATGTTTAAGTT TGTTTCACCTACGCATGAAGACATCACCAGCAGGGTCGTCTTTATTTCTAGTAGCTTATT TACAGCAAGCTTGTAACGTATGCTGAATTGCTGTGCCTCTGTAGAACACAGCATCTATGT GAATTGTTGACGTGGTTTGCCTTGATGGGTTCGTTGACTTGGTTTGTTGGATACTGA TTAAGGTGACTCTGCTGGGAGGCTTGGATTCTGGGGCCGGTGTTCTTTGCTCTCTGTCT AGGGTGGCGATTATTTCCCAACCCACTTGTTCCATTACACTCAAAACCTGCTATCAATTT ACAG

DOMAIN 1A-3 (3rd part of domain a)

INTRON 1A-3/1A-4 (SEQ ID NO:113)

TCTTTAGCCTCTTTATGCCAAAAGCTATATATTAATGTAGGACCCTACATATATTATTTC CAG

DOMAIN 1A-4 (4th part of domain a)

CTACGACAGCTTAAACCTGAATGGAATGACGCCAGAACAGCTGAAAACAGAACTAGACGA
ACGCCACTCCAAAGAACGTGCGTTTGCAAGCTTCCGACTCAGTGGCTTTGGGGGTTCTGC
CAACGTTGTTGTCTATGCATGTGTCCCTGATGATGATCCACGCAGTGATGACTACTGCGA
GAAAGCAGGCGACTTCTTCATTCTTGGGGGTCAAAGCGAAATGCCGTGGAGATTCTACAG
ACCCTTCTTCTATGATGTAACTGAAGCGGTACATCACCTTGGAGTCCCGCTAAGTGGCCA
CTACTATGTGAAAACAGAACTCTTCAGCGTGAATGGCACAGCACTTTCACCTGATCTTCT
TCCTCAACCAACTGTTGCCTACCGACCTGGGAAAGGTCACCTTGACC

INTRON 1A-4/1B (SEQ ID NO:114)

GTAAGTTGATTGTCTTAATATTGTTTTAATTTTTGCAGAAATTTGATTTTAAATTGTGTA AAAGGTTTCAATCGTGAAAACAAAACAATTCTCTATCTGTATACCCCTCAATACCAGTA TGATCACAAATCTAGGAAATATTACAATACTGCTTCATAGAGTAACTGCTGTTTGTGGCA GAGCTGGATACGAAGTTTCTGATAGTTCACAGCTACATGATAGTAAATGAACCTGTACAC ATCAACGGTTGATCATGAAAATTTTGTATGTGTGAAAGTGCTACCTGTATTAGTGAACGT GCTACCTGTATAACTGAAAGTGCTACCTGTATGACTGAAAGTGCTACCTGTATGCTGAAA GTGCTACCTGTATTAGTGAACGTGCTACCTGTATAACTGAAAGTGCTACCTGTATGACTG AAAGTGCTACCTGTATTAGTGAAAGTGCTACCTGTATGAGTGAACGTGCTACCTGTATAA CTGAAAGTGCTACCTGTATGACTGAAAGTGCTACCTGTATTAGTGAAAGTGCTGCCTGTA TTAGTGAAAGTGCTACCTGTATGACTGAGCGTGTTACCTGTATGACTGAACGTGCTACCT GTATTAGTGAAAGTGTAATCTGTATGAGTGAAAGTGCTACCTGTATTAGTGAAAGTGCTA CTACCTGTGTGACTGAAAGTGCTACCTGTATTAGTGAAAGTGCTACCTGTATGACTGAAC GTGCTACCTGTATTAGTGATAGTGTCACTGGTACCAACTGGATGTTCTCACTTCTTTGGC GAATATCTGGGCTCAAAACAGTTTTTCAGTATCATAGTCGTATCAGTTTGATTTGTATGT GCAGTGGAATCATTTTCGTCAAATAATCAAAACTGGTGTTGAACTGGCGTTCACGTTTTA TGGTTGTAAAACAAATTCTGTAAGTAAAGATATTTTAGGGATATCTGTATGACATGAACT GAATTGCTTAAGGTTAGCATGCCATGACAAATTGCTGAATGTCTGAGGATTGGTGGAGCA ATAAATCATTATTAAGACAAAAATCAGAAACGTCCATTTTCACTTTTAACAGTGTATCTG TCTGAATGCCCCCTACTTTTTGGAAGAGTATATATGAATTATCGGCAATATAAAACGTTA AATGGCAAATGTCGGGCATATGTCAGGACATTATTACCGCAGTTTATAGTCATATTTACC GGGTCTAGGACAATTGTCACCCCGACAATTGCCACCCGGACAATTGCCACCCAAAAATAA AATATACGTAAACAGAAAACAAATATTGCTTTCAGCCTTTATTGAGTTAGATAATGACAT TTATGTTGATAAATATGTCGTTTGATAATAATAATAACAATAATATAATATTACAATACT ATGTTGTAGGCAACACTTCGTCGGTAGGCCGTTAGGTAGTTATCATTAGGGCTGAGTATT GCGCCAAATTTCGTATTGCTATATACTGCGATACACGGTTACCTGTTTTGCAATACGTAA ACTTAGGCAAATATGACAGTTTTTCCATGATTATTTTCACGTTTCAATGCTTAAAATGGT CTTATCTGTTATCTCCTTGAAGGTTTAATAAAATAACAATAAACATAAATCATTATTGAA GATTACTATCCAAGAATGTGAAATTCACAAACACCTTGGGATAACACTGCAAAACGACTG TTCATGGGACGGACATGAAAAAGGTGAGTCCCATGTTAAACTGTTGAGAAAGTTTCCTAT ATTACTGTTCTCATATTTGGGACAACTGTGCAGATCGGTAGCATCCAAGCTCGTCTAAAT CGGTTTGATAAACCTTGTCAAATAACATGTTGTCTCAACATCCAAGCTCACCTAAACCTT GTCAATACCTGCATCTGAACAAATGTATATTTAAGACGATAGCATCCAAGCTCATCTTTA AAATGAATATTTTCTCTTTTTCTACCAAAACATTATTTGGTTGACAGTTGTCCTCCCTAT TATAGTAAAAAGAACTGGGTGGCAATTGTCCTAGGTGGCAATTGTCCGGATGGCAATTGT

#### DOMAIN 1B

CACCTGTGCATCATCGCCACGATGACGATCTTATTGTTCGAAAAAATATAGATCATTTGA CTCGTGAAGAGGAATACGAGCTAAGGATGGCTCTGGAGAGATTCCAGGCCGACACATCCG TTGATGGGTACCAGGCTACAGTAGAGTACCATGGCCTTCCTGCTCGTTGTCCACGACCAG GGCTGTTCGTTACCCAGGTGGAAGATGCTCTTGTACGGCGTGGATCGCCTATCGGTGTTC CTTATTGGGACTGGACAAAACCTATGACTCACCTTCCAGACTTGGCATCAAATGAGACGT ACGTAGACCCGTATGGACATACACATCATAATCCATTCTTCAATGCAAATATATCTTTTG AGGAGGGACACCATCACACGAGCAGGATGATAGATTCGAAACTGTTTGCCCCAGTCGCTT TTGGGGAGCATTCCCATCTGTTTGATGGAATCCTGTACGCATTTGAGCAGGAAGATTTCT GCGACTTTGAGATTCAGTTTGAGTTAGTCCATAATTCTATTCATGCGTGGATAGGCGGTT CCGAAGATTACTCCATGGCCACCCTGCATTACACAGCCTTTGACCCCATTTTCTACCTTC ATCATTCCAATGTCGATCGTCTATGGGCAATCTGGCAAGCTCTTCAAATCAGGAGACACA AGCCATATCAAGCCCACTGTGCACAGTCTGTGGAACAGTTGCCAATGAAGCCATTTGCTT TCCCATCACCTCTTAACAACAACGAGAAGACACATAGTCATTCAGTCCCGACTGACATTT ATGACTACGAGGAAGTGCTGCACTACAGCTACGATGATCTAACGTTTGGTGGGATGAACC TTGAAGAAATAGAAGAAGCTATACATCTCAGACAACAGCATGAACGAGTCTTCGCGGGAT ACCAACCACTCAAAGCTGGAGATATTGCCATTCTTGGTGGTGCCAAGGAAATGCCTTGGG CGTTTGACCGCTTGTATAAGGTCGAAATAACTGACTCATTGAAGACACTTTCTCTCGATG TCGATGGAGATTATGAAGTCACTTTTAAAATTCATGATATGCACGGAAACGCTCTTGATA CGGACCTGATTCCACACGCAGCAGTTGTTTCTGAGCCAGCTCACC

#### INTRON 1B/1C (SEO ID NO:115)

#### DOMAIN 1C

INTRON 1C/1D (SEQ ID NO:116)

GTACGTGGATTTGATTACATAGCAATGCTATATGATTTCAGTAATTACAACCTCAAGTCA
TGTAGCCGTTTTAGATTGCATTACATCAAACAGCATTGGATTAAATTGGGGGATTGTCCA
GGCCGCATTATGTTGCATTCCGAAAATAGTTTTGTGTCCAGTGTCCACGTTTAAAATTAAA
CCATTTTAATCATATTAGGGATAATTTTAATAGATGTTATAGTGCTTTATTTCATATTGT
TACAGTGGACAGTCACCAAGGACATATTTTACTCTATAGATACACAAACACCAATTAAAA
CCCTGCTTTGGAAAGTCTAACTTTTTCCCCACAG

#### DOMAIN 1D

GCACCCGTGATCGTGATAACTACGTTGAAGAAGTTACTGGGGCCAGTCATATCAGGAAGA ATTTGAACGACCTCAATACCGGAGAAATGGAAAGCCTTAGAGCTGCTTTCCTGCATATTC AGGACGACGGAACATATGAATCTATTGCCCAGTACCATGGCAAACCAGGCAAATGTCAAT TGAATGATCATAATATTGCGTGTTGTGTCCATGGTATGCCTACCTTCCCCCAGTGGCACA GACTGTATGTGGTTCAGGTGGAGAATGCTCTCCTAAACAGGGGATCTGGTGTGGCTGTTC ACTTCAATTCCCGACAACAGCGGTACGACCCTAACCCTTTCTTCAGGGGAAAGGTTACTT TTGAAAACGCAGTCACAACAAGGGACCCACAAGCCGGGCTCTTCAACTCAGATTATATGT ATGAGAATGTTTTACTTGCACTGGAGCAGGAAAATTATTGTGACTTTGAAATTCAGTTTG AGCTTGTTCATAACGCACTTCATTCCATGCTGGGAGGTAAAGGGCAGTACTCCATGTCCT CCCTGGACTATTCTGCGTTTGATCCCGTCTTCTTCCTACATCATGCCAACACGGACAGAC TGTGGGCAATCTGGCAGGAACTACAAAGATTCCGAGAACTGCCTTATGAAGAAGCGAACT GTGCAATCAACCTCATGCATCAACCACTGAAGCCGTTCAGTGATCCACATGAGAATCACG ACAATGTCACTTTGAAATACTCAAAACCACAGGACGGATTCGACTACCAGAACCACTTCG GTCATGAGGCGGGAACATTCTATATCCTCGGAGGCGAAACAGAGATGCCTTTTATCTTTG ACCGTTTGTATAAATTTGAAATCACCAAACCACTGCAACAGTTAGGAGTCAAGCTGCATG GTGGAGTTTTCGAACTGGAGCTTGAGATCAAGGCATACAACGGTTCCTATCTGGATCCCC ATACCTTTGATCCAACTATCATCTTTGAACCTGGAACAG

INTRON 1D/1E (SEQ ID NO:117)

GTAATGCCATCTTAATACAGTTCGTTCGTTAAATTATATATGTTCGTTTACAACACCATA CCTTGAATTGAGGTAATACATCACTTGATATTGATAATGTAATGGTAATTGTTCTTGTTT GTAAAACCGTTTCTGGGGTGTTTATTCACTATCCACCTGGTGGATAGTGAGTAAACACAT TCGGTTTAATATGGGTATCTAATGGACAGTGAAGTGTGCTGGCTAGGCAGATACCTTGGT TTCTGTGAATGGAGGTAGTAGAAAGGGGTTTTGATGATTGCAG

#### DOMAIN 1E

ATACCCATATCTTGGACCACGACCATGAGGAAGAGATACTTGTCAGGAAGAATATAATTG ATTTGAGCCCAAGGGAGAGGTTTCTCTAGTCAAAGCTTTGCAAAGAATGAAGAATGATC GCTCCGCTGATGGGTACCAAGCCATTGCCTCTTTCCATGCCCTGCCACCACTCTGTCCCA ATCCATCTGCAGCTCACCGTTATGCTTGCTGTGTCCATGGCATGGCTACATTTCCCCAGT GGCACAGACTGTACACTGTTCAGGTTCAGGATGCCCTGAGGAGACATGGTTCACTTGTTG CAACATTTTATCATCCAATCCGGAATATTAATATTTCAAATCCATTCCTCGGGGCTGACA TAGAATTTGAAGGACCGGGCGTTCATACAGAGAGGCACATAAATACTGAGCGCCTGTTTC ACAGTGGGGATCATGACGGATACCACAACTGGTTCTTCGAAACTGTTCTCTTTGCTTTGG AACAGGAAGATTACTGCGATTTTGAAATACAATTTGAGATAGCCCATAATGGCATCCACA CATGGATTGGTGGAAGCGCAGTATATGGCATGGGACACCTTCACTATGCATCATATGATC CAATTTTCTACATCCACCATTCACAGACGGACAGAATATGGGCTATTTGGCAAGAGCTGC AGAAGTACAGGGGTCTATCTGGTTCGGAAGCAAACTGTGCCATTGAACATATGAGAACAC CCTTGAAGCCTTTCAGCTTTGGGCCACCCTACAATTTGAATAGTCATACGCAAGAATATT CAAAGCCTGAGGACACGTTTGACTATAAGAAGTTTGGATACAGATATGATAGTCTGGAAT TGGAGGGGCGATCAATTTCTCGCATTGATGAACTTATCCAGCAGAGACAGGAGAAAGACA GAACTTTTGCAGGGTTCCTCCTTAAAGGTTTTTGGTACATCCGCATCTGTGTCATTGCAAG TTTGCAGAGTTGATCACACCTGTAAAGATGCGGGCTATTTCACTATTCTGGGAGGATCAG CCGAAATGCCATGGGCATTCGACAGGCTTTATAAGTATGACATTACTAAAACTCTTCACG ACATGAACCTGAGGCACGAGGACACTTTCTCTATAGACGTAACTATCACGTCTTACAATG GAACAGTACTCTCGGGAGACCTCATTCAGACGCCCTCCATTATATTTGTACCTGGACGCC

INTRON 1E/1F-1 (SEQ ID NO:118)

GTGAGTACCTGTTTGCACTAAGACTTCTGTAGGCTAAAAGTGTAAGAAATATCAATTAAT TTCAATTCACCCAAACTTGAAAACGGTACCTATATAGGTTAACTTTTTGTCTACAGTAAA CTGAACATACCTACACATTTCATGAAATGATCTCTCAATATTTTCCACCAACAG

DOMAIN 1F-1 (1st part of domain f)

ATAAACTCAACTCACGGAAACATACACCTAACAGAGTCCGCCATGAGCTAAGTAGCCTTAGTTCCCGTGACATAGCAAGCTTGAAGGCAGCTTTGACAAGCCTTCAACATGATAATGGGACTGATGGTTATCAAGCTATTGCTGCCTTCCATGGCGTTCCTGCGCAGTGCCACGAGCCATCTGGACGTGAG

INTRON 1F-1/1F-2 (SEQ ID NO:119)

#### 15 / 44

DOMAIN 1F-2 (2nd part of domain f)

ATCGCCTGTTGCATCCACGGCATGGCGACGTTTCCTCACTGGCACCGGTTGTACACTCTG CAGTTGGAGCAAGCGCTGCGCAGACACGGGTCCAGTGTTGCTGTTCCATACTGGGACTGG-ACCAAGCCAATCACCGAACTGCCACACATTCTGACAGACGGAGAATATTATGACGTTTGG CAAAATGCCGTCTTGGCCAATCCGTTTGCAAGAGGTTATGTGAAAATTAAAGATGCATTT ACGGTGAGAAATGTCCAGGAAAGTCTGTTCAAAATGTCAAGTTTTGGAAAGCACTCGCTT CTGTTTGACCAGGCTTTGTTGGCTCTTGAACAACTGACTACTGTGACTTCGAAGTTCAG TTTGAAGTGATGCATAACACGATCCATTATCTCGTAGGAGGGCGTCAAACGTACGCCTTC TCCTCTCTCGAGTATTCCTCATACGATCCAATCTTCTTTATTCACCACTCGTTTGTTGAC AAAATATGGGCTGTATGGCAAGAACTGCAAAGCAGGAGACATCTACAGTTTAGAACAGCT GATTGTGCTGTGGGCCTCATGGGTCAGGCAATGAGGCCTTTCAACAAGGATTTCAACCAC AACTCGTTCACCAAGAAGCACGCAGTCCCTAATACAGTATTTGATTATGAAGATCTTGGC TATAACTATGACAACCTTGAAATCAGTGGTTTAAACTTAAATGAGATCGAGGCGTTAATA TCGGCTGATATACATCTGGAAATTTGCAAGACATCGGAAAACTGCCATGATGCTGGTGTG ATTTTCATCCTTGGAGGTTCTGCAGAGATGCATTGGGCATACAACCGCCTCTACAAGTAT GACATTACAGAAGCATTGCAGGAATTTGACATCAACCCTGAAGATGTTTTCCATGCTGAT GAACCATTTTTCCTGAGGCTGTCGGTTGTTGCTGTGAATGGAACTGTCATTCCATCGTCT CATCTTCACCAGCCAACGATAATCTATGAACCAGGCGAAG

INTRON 1F-2/1G-1 (SEQ ID NO:120)

GTGAGATATTGCAAATTGAATGTTGTCCAGATGCGTTGTTTACATTTATATGCTTGGAA
TTGTCCTGAACGAATACAGTGGAATAACCAAAAGCTGAAAAATAAAAAGATATATACTTC
ATTCTGAATTTGTCAGTATTGCTGACCCAAAAACACGTTATCCATGTCGACACTATATTT
GCCTTTCTGAATCTGAGACTGCGTTATGTTTCTAATAATCACGAAATATGGTATACAGGT
TGTGTATCTGTAGAATACCCAAGGCAGAATTTAAAGGGTCACACCCTGTTTAATACAG

DOMAIN 1G-1 (1st part of domain g)

ATCACCATGACGACCATCAGTCGGGAAGCATAGCAGGATCCGGGGTCCGCAAGGACGTGA ACACCTTGACTAAGGCTGAGACCGACAACCTGAGGGAGGCGCTGTGGGGTGTCATGGCAG ACCACGGTCCCAATGGCTTTCAAGCTATTGCTGCTTTCCATGGAAAACCAGCTTTGTGTC CCATGCCTGATGGCCACAACTACTCATGTTGTACTCACG

INTRON 1G-1/1G-2 (SEQ ID NO:121)

TGTGTCTATGTGTGACATGCAATACATGCTGTGATACTCACTAGCTGCGTCTATCGAC CAG

DOMAIN 1G-2 (2nd part of domain g)

· ;

INTRON 1G-2/1G-3 (SEQ ID NO:122)

DOMAIN 1G-3 (3rd part of domain g)

INTRON 1G-3/1H (SEQ ID NO:123)

#### DOMAIN 1H

TGCACAGAGGCGGAAACCACGAAGATGAACACCATGATGACAGACTCGCAGATGTCCTGA TCAGGAAGAAGTTGACTTCCTCTCCCTGCAAGAGGCCAACGCAATTAAGGATGCACTGT ACAAGCTCCAGAATGACGACAGTAAAGGGGGGCTTTGAGGCCATAGCTGGCTATCACGGGT ATCCTAATATGTGTCCAGAAAGAGGTACCGACAAGTATCCCTGCTGTGTCCACGGAATGC CCGTGTTCCCCCACTGGCACCGCCTGCATACCATTCAGATGGAGAGAGCTCTGAAAAACC ATGGCTCTCCAATGGGCATTCCTTACTGGGATTGGACAAAGAAGATGTCGAGTCTTCCAT CTTTCTTTGGAGATTCCAGCAACAACAACCCTTTCTACAAATATTACATCCGGGGCGTGC AGCACGAAACAACCAGGGACATTAATCAGAGACTCTTTAATCAAACCAAGTTTGGTGAAT TTGATTACCTATATTACCTAACTCTGCAAGTCCTGGAGGAAAACTCGTACTGTGACTTTG AAGTTCAGTATGAGATCCTCCATAACGCCGTCCACTCCTGGCTTGGAGGAACTGGAAAGT ATTCCATGTCTACCCTGGAGCATTCGGCCTTTGACCCTGTCTTCATGATTCACCACTCGA GTTTGGATAGAATCTGGATCCTTTGGCAGAAGTTGCAAAAGATAAGAATGAAGCCTTACT ACGCATTGGATTGTGCTGGCGACAGACTTATGAAAGACCCCCTGCATCCCTTCAACTACG AAACCGTTAATGAAGATGAATTCACCCGCATCAACTCTTTCCCAAGCATACTGTTTGACC TTGAAGAGGTAATTCAGGAATTAAGAAACAAAGATCGCATATTTGCTGGTTTTTGT ACGAAGAATATGCAGGAGAATTTGCAGTTTTGGGAGGTGAGAAGGAGATGCCGTGGGCAT ATGAAAGAATGCTGAAATTGGACATCTCCGATGCTGTACACAAGCTTCACGTGAAAGATG AAGACATCCGTTTTAGAGTGGTTGTTACTGCCTACAACGGTGACGTTGTTACCACCAGGC TGTCTCAGCCATTCATCGTCCACCGTCCAGCCCATGTGGCTCACGACATCTTGGTAATCC CAGTAGGTGCGGGCCATGACCTTCCGCCTAAAGTCGTAGTAAAGAGCGGCACCAAAGTCG AGTTTACACCAATAGATTCGTCGGTGAACAAAGCAATGGTGGAGCTGGGCAGCTATACTG CTATGGCTAAATGCATCGTTCCCCCTTTCTCTTACCACGGCTTTGAACTGGACAAAGTCT ACAGCGTCGATCACGGAGACTACTACATTGCTGCAGGTACCCACGCGTTGTGTGAGCAGA ACCTCAGGCTCCACATCCACGTGGAACACGAGTAG

3'UTR

**TTCACAG** 

INTRON 3'UTR (SEO ID NO:124)

GTGAGGAGAGGCCCCAGGCTAGCAGGGCAATGGATGAAGGAAATAGGGGCAAAGGGAAT
AGCAGTTACACCATCGACATTTCCAACCTCCTCAGAAACTAATATATAGCCTTAATACAA
CCAGCCAAGACTCAACGGGCAGCCGGGGTGGGGGGATTTGGTGGTCGCTGTTTCAGACCA
GGGTGCAAAATATCAGTGCGCAAATCAACATGTTGCGTGTCAGACACTGACACAGCAGTC
ATTGAACCTGCAGACCCATAACAGGAAAATGGGGCAGATACGATCAAAGACAGTGTAAAA
TAGGGATAAGTAGGCATATGCAACCACCTGATGGAAATGAAAAGGGGTAAGTTTAAACCC
CGGCTACCAAAGGTCCAATGGTTCCTTAACCCAGCTTACGCTATCCCTCTAATTTCAGTA
TTGAGCTGATTTCTGTCGAGTTCATGTAAACTGTATACTTTCTGTATTATTACAG

3´UTR

GTTGCTATGCCGACTGCGCTATATTGGTGAACGAGACGATGAGGACATCTCTGAAAGAGT
TCGCCAAGTGATGTTGAGGTCACGGAAGTATTGTTGAGCTAACAATATGATGATTTCAAA
ATGACTTGGCGCTCTAGGACAAAGACATAATTCATCAGCACCCCTGTGCACCAACTCTTTG
TTTGCTGCAAACGTCTGACAAGCGACACGTCAATCAACAAGCTGTTCAAAACTCAAGTGGA
TGTAACTAGAATCGTTGGGCCATCGTTCACAAAGTATTGACAGATGTCACACATGATGGC
GAGAAACACTTTAGAACTTTTAATGACCTAGAGTGACTTGTAAATATGTAAATATATTCT

# 18 / 44

# Figure 5

# Primary structure of the HtH1 protein

#### SIGNAL PEPTIDE

LVQFLLVALVVGAGA

### DOMAIN A

DNVVRKDVSHLTVDEVQALHGALHDVTASTGPLSFEDITSYHAAPASCDYKGRKIACCVHGMPSFP FWHRAYVVQAERALLSKRKTVGMPYWDWTQTLTHLPSLVTEPIYIDSKGGKAQTNYWYRGEIAFIN KKTARAVDDRLFEKVEPGHYTHLMETVLDALEQDEFCKFEIQFELAHNAIHYLVGGKFEYSMSNLE YTSYDPIFFLHHSNVDRLFAIWQRLQELRGKNPNAMDCAHELAHQQLQPFNRDSNPVQLTKDHSTP ADLFDYKQLGYSYDSLNLNGMTPEQLKTELDERHSKERAFASFRLSGFGGSANVVVYACVPDDDPR SDDYCEKAGDFFILGGQSEMPWRFYRPFFYDVTEAVHHLGVPLSGHYYVKTELFSVNGTALSPDLL POPTVAYRPGK

#### DOMAIN B

GHLDPPVHHRHDDDLIVRKNIDHLTREEEYELRMALERFQADTSVDGYQATVEYHGLPARCPRPDA KVRFACCMHGMASFPHWHRLFVTQVEDALVRRGSPIGVPYWDWTKPMTHLPDLASNETYVDPYGHT HHNPFFNANISFEEGHHHTSRMIDSKLFAPVAFGEHSHLFDGILYAFEQEDFCDFEIQFELVHNSI HAWIGGSEDYSMATLHYTAFDPIFYLHHSNVDRLWAIWQALQIRRHKPYQAHCAQSVEQLPMKPFA FPSPLNNNEKTHSHSVPTDIYDYEEVLHYSYDDLTFGGMNLEEIEEAIHLRQQHERVFAGFLLAGI GTSALVDIFINKPGNQPLKAGDIAILGGAKEMPWAFDRLYKVEITDSLKTLSLDVDGDYEVTFKIH DMHGNALDTDLIPHAAVVSEPAH

#### DOMAIN C

PTFEDEKHSLRIRKNVDSLTPEETNELRKALELLENDHTAGGFNQLGAFHGEPKWCPNPEAEHKVA CCVHGMAVFPHWHRLLALQAENALRKHGYSGALPYWDWTRPLSQLPDLVSHEQYTDPSDHHVKHNP WFNGHIDTVNQDTTRSVREDLYQQPEFGHFTDIAQQVLLALEQDDFCSFEVQYEISHNFIHALVGG TDAYGMASLRYTAYDPIFFLHHSNTDRIWAIWQSLQKYRGKPYNTANCAIESMRRPLQPFGLSSAI NPDRITREHAIPFDVFNYRDNLHYVYDTLEFNGLSISQLDRELEKIKSHERVFAGFLLSGIKKSAL VKFEVCTPPDNCHKAGEFYLLGDENEMAWAYDRLFKYDITQVLEANHLHFYDHLFIRYEVFDLKGV SLGTDLFHTANVVHDSGT

#### DOMAIN D

GTRDRDNYVEEVTGASHIRKNLNDLNTGEMESLRAAFLHIQDDGTYESIAQYHGKPGKCQLNDHNI ACCVHGMPTFPQWHRLYVVQVENALLNRGSGVAVPYWEWTAPIDHLPHFIDDATYFNSRQQRYDPN PFFRGKVTFENAVTTRDPQAGLFNSDYMYENVLLALEQENYCDFEIQFELVHNALHSMLGGKGQYS MSSLDYSAFDPVFFLHHANTDRLWAIWQELQRFRELPYEEANCAINLMHQPLKPFSDPHENHDNVT LKYSKPQDGFDYQNHFGYKYDNLEFHHLSIPSLDATLKQRRNHDRVFAGFLLHNIGTSADITIYIC LPDGRRGNDCSHEAGTFYILGGETEMPFIFDRLYKFEITKPLQQLGVKLHGGVFELELEIKAYNGS YLDPHTFDPTIIFEPGT

## DOMAIN E

DTHILDHDHEEEILVRKNIIDLSPRERVSLVKALQRMKNDRSADGYQAIASFHALPPLCPNPSAAH RYACCVHGMATFPQWHRLYTVQVQDALRRHGSLVGIPYWDWTKPVNELPELLSSATFYHPIRNINI SNPFLGADIEFEGPGVHTERHINTERLFHSGDHDGYHNWFFETVLFALEQEDYCDFEIQFEIAHNG IHTWIGGSAVYGMGHLHYASYDPIFYIHHSQTDRIWAIWQELQKYRGLSGSEANCAIEHMRTPLKPFSFGPPYNLNSHTQEYSKPEDTFDYKKFGYRYDSLELEGRSISRIDELIQQRQEKDRTFAGFLLKGFGTSASVSLQVCRVDHTCKDAGYFTILGGSAEMPWAFDRLYKYDITKTLHDMNLRHEDTFSIDVTITSYNGTVLSGDLIQTPSIIFVPGR

## DOMAIN F

HKLNSRKHTPNRVRHELSSLSSRDIASLKAALTSLQHDNGTDGYQAIAAFHGVPAQCHEPSGREIA CCIHGMATFPHWHRLYTLQLEQALRRHGSSVAVPYWDWTKPITELPHILTDGEYYDVWQNAVLANP FARGYVKIKDAFTVRNVQESLFKMSSFGKHSLLFDQALLALEQTDYCDFEVQFEVMHNTIHYLVGG RQTYAFSSLEYSSYDPIFFIHHSFVDKIWAVWQELQSRRHLQFRTADCAVGLMGQAMRPFNKDFNH NSFTKKHAVPNTVFDYEDLGYNYDNLEISGLNLNEIEALIAKRKSHARVFAGFLLFGLGTSADIHL EICKTSENCHDAGVIFILGGSAEMHWAYNRLYKYDITEALQEFDINPEDVFHADEPFFLRLSVVAV NGTVIPSSHLHQPTIIYEPGE

### DOMAIN G

DHHDDHQSGSIAGSGVRKDVNTLTKAETDNLREALWGVMADHGPNGFQAIAAFHGKPALCPMPDGH NYSCCTHGMATFPHWHRLYTKQMEDAMRAHGSHVGLPYWDWTAAFTHLPTLVTDTDNNPFQHGHID YLNVSTTRSPRDMLFNDPEHGSESFFYRQVLLALEQTDFCKFEVQFEITHNAIHSWTGGHSPYGMS TLDFTAYDPLFWLHHSNTDRIWAVWQALQEYRGLPYNHANCEIQAMKTPLRPFSDDINHNPVTKAN AKPLDVFEYNRLSFQYDNLIFHGYSIPELDRVLEERKEEDRIFAAFLLSGIKRSADVVFDICQPEH ECVFAGTFAILGGELEMPWSFDRLFRYDITKVMKQLHLRHDSDFTFRVKIVGTDDHELPSDSVKAP TIEFEPG

# DOMAIN H

VHRGGNHEDEHHDDRLADVLIRKEVDFLSLQEANAIKDALYKLQNDDSKGGFEAIAGYHGYPNMCP ERGTDKYPCCVHGMPVFPHWHRLHTIQMERALKNHGSPMGIPYWDWTKKMSSLPSFFGDSSNNNPF YKYYIRGVQHETTRDINQRLFNQTKFGEFDYLYYLTLQVLEENSYCDFEVQYEILHNAVHSWLGGT GKYSMSTLEHSAFDPVFMIHHSSLDRIWILWQKLQKIRMKPYYALDCAGDRLMKDPLHPFNYETVN EDEFTRINSFPSILFDHYRFNYEYDNMRIRGQDIHELEEVIQELRNKDRIFAGFVLSGLRISATVK VFIHSKNDTSHEEYAGEFAVLGGEKEMPWAYERMLKLDISDAVHKLHVKDEDIRFRVVVTAYNGDV VTTRLSQPFIVHRPAHVAHDILVIPVGAGHDLPPKVVVKSGTKVEFTPIDSSVNKAMVELGSYTAM AKCIVPPFSYHGFELDKVYSVDHGDYYIAAGTHALCEQNLRLHIHVEHE

# Figure 6

# Genomic sequence of the HtH2 gene

DOMAIN 2A-1 (1st part of domain a) [domain a, parts 1-4: SEQ ID NO:156]

GGTCTTCCGTACTGGGACTGGACGCAGCATCTGACTCAACTCCCAGATCTGGTGTCAGACCCCTTG
TTTGTCGACCCGGAAGGAGGAAAG

INTRON 2A-1/2A-2 (SEQ ID NO:125)

CCGCCCTACTGGGGATCACAGGGAATGTATGTCAATGGTTGAAGAAAGGAGCAGTGGGTTACAACG CCGCGTTCAAAGTCATGGCAGTTTCATAGCGCATTGTGCGCGCGTGTGTATCTGTGTGCGCGCGTG TGTGCTTGCGTGCGTGTGAGTGAGTCCGCTTGTGCATTTGTACTAGCACAGACTAATGCTGGTTCT AGAGAGCCTACTGATAAATGTTTACATTAAGATCTTTACAGTATACTGAGATTCGAGCCCAGACCA GCGGAACACCAGGCAGGGTAACAACAAATAACGCCTTTCCACACAACCGACGCAGCCTAAAGTGGC TCTGATAGGCTGATACCGGTGTATTCTTAGAACTTGTAATTTGTGCTTTGCCATAATACATGTACT TCAGTTAACTGTAATACAGCATAAGACTGGACCGGTGTTTACGACGCAATGAGCAATAATTACTCT  ${\tt TCTCGTTTGTGTCAACGTATTCATAATCATTCTCATGCATCTGTTAGCTCAGATATTTTGATGTTT}$ TACCTGGCGAGACAATAAGATCTTACTAGTGCTGCCACTTCAGTATGGTGTCCCCGATGGTGTCTG GTGTATGGGTGTGTTTGGCGTCAGTTGTTACTGGAAAAGTCAGCTCTAATTATGTCTTTATGTGGT TGACGCTTAAACGTTAGATGAATAAGGACTATATTGTGTTGTATAACATTTCTATAACCTCCTTTC TATATCATTTAG

DOMAIN 2A-2 (2nd part of domain a)

GCCCATGACAACGCATGGTATCGTGGAAACATCAAGTTTGAGAATAAGAAGACTGCAAGAGCTGTTGACGATCGCCTTTTCGAGAAGGCTGGTTGACCAGGAGAGATTCTCGAGACACGCTGTTTGAACAGGATGAATTCTCGAGATCCAGTTTGAACAGGATGAATTCTGCAACTTCGAGATCCAGTTTGAGTTGGCTCACAACGCTATCCACTACCTGGTTGGCGGCCGTCACAC

INTRON 2A-2/2A-3 (SEO ID NO:126)

DOMAIN 2A-3 (3rd part of domain a)

INTRON 2A-3/2A-4 (SEQ ID NO:127)

DOMAIN 2A-4 (4th part of domain a)

GTATGATGACCTTGACCCTGAACGGTATGACCCCAGAGGAATTGAACTCATATCTGCATGAACGGTC
AGGCAAGGAGGGGGTGTTCGCAAGCTTCCGACTCTCAGGTTTTTGGCGGCTCTGCTAACGTTGTTGT
CTACGCATGCCGTCCTGCCCACGATGAAATGGCTGTCGATCAGTGCGACAAAGCCGGCGACTTCTT
TGTGTTGGGCGGACCCACCGAGATGCCCTGGAGGTTTTACAGAGCATTCCACTTCGACGTCACCGA
CAGCATCGACAACATCGACAAGGACCGCCACGGCCACTATTATGTAAAGGCGGAATTATTCAGTGT
AAATGGAAGTGCGCTACCGAATGATCTCCTGCCTCAACCCACCATCTCACACAGGCCAGCCCGCGG
ACACGTTGATG

INTRON 2A-4/2B (SEQ ID NO:128)

#### DOMAIN 2B

INTRON 2B/2C (SEQ ID NO:129)

#### DOMAIN 2C

TTGACCATCAGGACCCTCATCAGGACACAATCATCAGGAAAAATGTTGATAATCTTACACCCGAGG AAATTAATTCTCTGAGGAGGGCAATGGCAGACCTTCAATCAGACAAAACCGCCGGTGGATTCCAGC AAATTGCTGCTTTTCACGGGGAACCCAAATGGTGCCCAAGTCCCGATGCTGAGAAGAAGTTCTCCT GCTGTGTCCATGGAATGGCTGTCTTCCCTCACTGGCACAGACTCCTGACCGTGCAAGGCGAGAATG  $\verb|CCCTGAGAAAGCATGGATGTCTCGGAGCTCTCCCCTACTGGGACTGGACTCGGCCCCTGTCTCACC| \\$ TACCTGATTTGGTAAGTCAGCAGAACTACACCGATGCCATATCCACCGTGGAAGCCCGAAACCCCT AAGCTCCCGGATTTGGTCATTATACTGGGGTCGCTAAGCAAGTGCTTCTGGCTTTGGAGCAGGATG ACTTCTGTGATTTTGAAGTCCAGTTTGAGATAGCTCACAATTTCATCCACGCTCTTGTCGGCGGAA  ${\tt GCGAGCCATATGGTATGGCGTCACTCCGTTACACTACTTATGATCCAATTTTCTACCTCCATCATT}$  $\verb|CTAACACTGACAGACTCTGGGCTATATGGCAGGCTCTACAAAAGTACAGGGGCAAACCTTACAATT| \\$ ACCCGGATGATGAGACAAGACAGCATGCTGTTCCTTTCAGTGTCTTTGATTACAAGAACAACTTCA ATTATGAATATGACACCCTTGACTTCAACGGACTATCAATCTCCCAGCTGGACCGTGAACTGTCAC GGAGAAAGTCTCATGACAGAGTATTTGCCGGATTTTTTGCTGCATGGTATTCAGCAGTCTGCACTAG TTAAATTCTTTGTCTGCAAATCAGATGATGACTGTGACCACTATGCTGGTGAATTCTACATCCTTG GTGATGAAGCTGAAATGCCATGGGGCTATGATCGTCTTTACAAATATGAGATCACTGAGCAGCTCA ATGCCCTGGATCTACACATCGGAGATAGATTCTTCATCAGATACGAAGCGTTTGATCTTCATGGTA CAAGTCTTGGAAGCAACATCTTCCCCAAACCTTCTGTCATACATGACGAAGGGGCAG

INTRON 2C/2D (SEQ ID NO:130)

GTGAGAACATTGATAATAGTTCAAATGAAGTATATCCGATTCAAGCTGTCGATACAAGATGAGATA CATAATCACAATGTTTGTATTAGATATCTCTCTTAATTTAATGCCGCTTTTATCAATATTCGAGCA ATCCTTCAGCAACATACACCAGCAAATGTTTCATCAACAGACTATATTTAATATTTTAAAAAT CCTTCTCTGTTGTTATAAATACTTAAAGTATCGAATTCCTTGAATGCGTCTTCTCTGCAGCATATA GTTAAGTTGTTGTTGTTCTCTGTCAG

## DOMAIN 2D

AAGATCTGTCAAAGGGAGAAGTAGAGAGCCTAAGGTCTGCCTTCCTGCAACTTCAGAACGACGAG TCTATGAGAATATTGCCAAATTCCACGGCAAGCCTGGGTTGTGTGATGATAACGGTCGCAAGGTTG CCTGTTGTGTCCATGGAATGCCCACCTTCCCCCAGTGGCACAGACTCTATGTCCTCCAGGTGGAGA ATGCTTTGCTGGAGAGAGGATCTGCCGTCTCTGTGCCATACTGGGACTGGACTGAAACATTTACAG AGCTGCCATCTTTGATTGCTGAGGCTACCTATTTCAATTCCCGTCAACAAACGTTTGACCCTAATC CTTTCTTCAGAGGTAAAATCAGTTTTGAGAATGCTGTTACAACACGTGATCCCCAGCCTGAGCTGT ACGTTAACAGGTACTACCAAAACGTCATGTTGGCTTTTGAACAGGACAACTACTGCGACTTCG AGATACAGTTTGAGATGGTTCACAATGTTCTCCATGCTTGGCTTGGTGGAAGAGCTACTTATTCTA TGTGGGCCATCTGGCAGGAGCTGCAGAGGTACAGGAAGAAGCCATACAATGAAGCGGATTGTGCCA TTAACCTAATGCGCAAACCTCTACATCCCTTCGACAACAGTGATCTCAATCATGATCCTGTAACCT TTAAATACTCAAAACCCACTGATGGCTTTGACTACCAGAACAACTTTGGATACAAGTATGACAACC TTGAGTTCAATCATTTCAGTATTCCCAGGCTTGAAGAAATCATTCGTATTAGACAACGTCAAGATC GTGTGTTTGCAGGATTCCTCCTTCACAACATTGGGACATCCGCAACTGTTGAGATATTCGTCTGTG TCCCTACCACCAGCGGTGAGCAAAACTGTGAAAACAAAGCCGGAACATTTGCCGTACTCGGAGGAG AAACAGAGATGGCGTTTCATTTTGACAGACTCTACAGGTTTGACATCAGTGAAACACTGAGGGACC TCGGCATACAGCTGGACAGCCATGACTTTGACCTCAGCATCAAGATTCAAGGAGTAAATGGATCCT ACCTTGATCCACACATCCTGCCAGAGCCATCCTTGATTTTTGTGCCTGGTTCAA

INTRON 2D/2E (SEQ ID NO:131)

GTAAGAAGTTTCACTGTCTAAATCTTTTTTTTATGATAGAGGGTAGAGAAGTGGAGACAATGTGAC AATATATTGAATAAAGTTGTTTAAAATTTATAACTCTCATAAGTTCATATTATGCTGAAGCTGTAG CCATCTATAACTGTGTAACATGAAATGTTAAGACATTAACCTAAATACTTCAGCTGATAACAAAAC AATGTTAATACATACGTCAATGTAACATTTTCTTATCTTTAGGTTATAGCATAAACACTTCAGAGA TACAGTGACGAAAACCTCTATTTAAATATTTCAG

#### DOMAIN 2E

GTTCTTTCCTGCGTCCTGATGGGCATTCAGATGACATCCTTGTGAGAAAAGAAGTGAACAGCCTGA CAACCAGGGAGACTGCATCTCTGATCCATGCTCTGAAAAGTATGCAGGAAGACCATTCACCTGATG GGTTCCAAGCCATTGCCTCTTTCCATGCCCTGCCACCACTCTGCCCTTCACCATCTGCAACTCACC GTTATGCTTGCTGTGTCCACGGCATGGCTACATTTCCCCAGTGGCACAGACTGTACACTGTACAGT TCCAGGATGCACTGAGGAGACATGGAGCTGCAGTAGGTGTACCGTATTGGGATTGGCTGCGACCGC AGTCTCACCTACCAGAGCTTGTCACCATGGAGACATACCATGATATTTGGAGTAACAGAGATTTCC TTGCAGACAAACTTTTTGTCAAAGGTGGACACGTTTTTGATAACTGGTTCTTCAAACAAGCCATCC TAGCGCTTGAGCAGGAAAACTACTGTGACTTTGAGATTCAGTTTGAAATTCTTCACAACGGCGTTC ACACGTGGGTCGGAGGCAGTCGTACCCACTCTATCGGACATCTCCATTACGCATCCTACGACCCTC TTTTCTACCTCCACCATTCCCAGACAGACCGTATTTGGGCAATCTGGCAAGAACTCCAGGAACAGA GAGGGCTCTCAGGTGATGAGGCTCACTGTGCTCTCGAGCAAATGAGAGAACCATTGAAGCCTTTCA GCTTCGGCGCTCCTTATAACTTGAATCAGCTAACACAGGATTTCTCCCGACCCGAGGACACCTTCG ACTACAGGAAGTTTGGTTATGAATATGACAATTTAGAATTCCTAGGAATGTCAGTTGCTGAACTGG ATCAATACATTATTGAACATCAAGAAAATGATAGAGTATTCGCTGGGTTCCTGTTGAGTGGATTCG GAGGTTCCGCATCAGTTAATTTCCAGGTTTGTAGAGCTGATTCCACATGTCAGGATGCTGGGTACT TCACCGTTCTTGGTGGCAGTGCTGAGATGGCGTGGGCATTTGACAGGCTATACAAATATGACATTA CTGAAACTCTGGAGAAAATGCACCTTCGATATGATGATGACTTCACAATCTCTGTCAGTCTGACCG CCAACAACGGAACTGTCCTGAGCAGCAGTCTAATCCCAACACCGAGTGTCATATTCCAGCGGGGAC ATC

INTRON 2E/2F-1 (SEQ ID NO:132)

GTAAGTAGTAAACTGCTCAGATTGTTTTCATAATTACTCCACTATTAAGTAAAAAGTACTAGTAAT TCAATAGTACTGTTCACAGAGAAATGTAACACAATAGACCACAGAGTCCATTTGTTAAACGCCTTT GGCTTGGTAAGTCTGAGATTTTGGTGACTGATGGAAAGCTAAAATATATTTTGACAG

DOMAIN 2F-1 (1st part of domain f)

INTRON 2F-1/2F-2 (SEQ ID NO:133)

DOMAIN 2F-2 (2nd part of domain f)

ATCGCATGTTGCATTCACGGTATGCCGACCTTCCCCCAGTGGCACAGACTGTACACCCTGCAGTTG GAGATGGCTCTGAGGAGACATGGATCATCTGTCGCCATCCCCTACTGGGACTGGACAAAGCCTATC t TCCGAACTCCCCTCGCTCTTCACCAGCCCTGAGTATTATGACCCATGGCATGATGCTGTGGTAAACAACCCATTCTCCAAAGGTTTTGTCAAATTTGCAAATACCTACACAGTAAGAGACCCACAGGAGATG CTGTTCCAGCTTTGTGAACATGGAGAGTCAATCCTCTATGAGCAAACTCTTCTTGCTCTAGAGCAA  ${\tt ACCGACTACTGTGATTTTGAGGTACAGTTTGAGGTCCTCCATAACGTGATCCACTACCTTGTTGGC}$ GGACGTCAGACCTACGCATTGTCTTCTCTGCATTATGCATCCTACGACCCATTCTTCTTTATACAC CATTCCTTTGTGGATAAGATGTGGGTAGTATGGCAAGCTCTTCAAAAGAGGAGGAAACTTCCATAC AAGCGAGCTGACTGTCCTGTCAACCTAATGACTAAACCAATGAGGCCATTTGACTCCGATATGAAT CAGAACCCATTCACAAAGATGCACGCAGTTCCCAACACTCTATGACTACGAGACACTGTACTAC AGCTACGATAATCTCGAAATAGGTGGCAGGAATCTCGACCAGCTTCAGGCTGAAATTGACAGAAGC AGAAGCCACGATCGCGTTTTTGCTGGATTCTTGCTTGGTGGAATCGGAACTTCTGCTGATGTCAGG TTTTGGATTTGTAGAAATGAAAATGACTGCCACAGGGGTGGAATAATTTTCATCTTAGGTGGAGCC  ${\tt AAGGAAATGCCATGGTCATTTGACAGAAACTTCAAGTTTGATATCACCCATGTACTCGAGAAAGCT}$ GGCATTAGCCCAGAGGACGTGTTTGATGCTGAGGAGCCATTTTATATCAAGGTTGAGATCCATGCT GTTAACAAGACCATGATACCATCGTCTGTGATCCCAGCCCCAACTATCATCTATTCTCCTGGGGAA G

INTRON 2F-2/2G-1 (SEQ ID NO:134)

DOMAIN 2G-1 (1st part of domain g)

INTRON 2G-1/2G-2 (SEQ ID NO:135)

DOMAIN 2G-2 (2nd part of domain g)

GTATGGCCTCCTTCCCACACTGGCACAGACTGTATGTGAAGCAGATGGAAGACGCCCTGGCTGACC ACGGATCACATATCGGCATCCCTTACTGGGACTGGACAACTGCCTTCACAGAGTTACCCGCCCTTG TCACAGACTCCGAGAACAATCCCTTCCATGAG

INTRON 2G-2/2G-3 (SEQ ID NO:136)

DOMAIN G-3 (3rd part of domain g)

INTRON 2G-3/2H (SEQ ID NO:137)

GTATGTTATCTTATTATCAAATGTGTAATCAGATACTGGAGACGTTTTCATATTAACTTGGTCAGC
ATTAGTTGATGATGATTTTGGTGCGATATTGACGACAAGGAGTTAAGCATTTAACACGTTCAACACATCT
TTAATCTGATATGAGAAGGGAATAAATTGATCCAGTATTGATGATTGAAGTTAACAGTGAA
AGATATACCAGTTTTGATAATCGTATAAAACAGTAGCAGAATTGTATCGTGAAAACTAAATGTGGG
AAGGCGAACGCCAAGCAGATTTTAGATTACGATCGTGTGCTAGAATAATTCACAATAACCCAGACG
TCGGAAATGTGGTTGTCTATGGCAATAGTTACGATTAATTGCTAACATGCACGATTTACCTATTTC
AG

#### DOMAIN 2H

CCCACAGAGGACCAGTTGAAGAAACAGAAGTCACTCACCAAAATACTGACGGCAATGCACACTTCC ATCGTAAGGAAGTTGATTCGCTGTCCCTGGATGAAGCAAACAACTTGAAGAATGCCCTTTACAAGC TACAGAACGACCACAGTCTAACAGGATACGAAGCAATCTCTGGTTACCATGGATACCCGAATCTGT GTCCGGAAGAGGCGATGACAAATACCCCTGCTGCGTCCACGGAATGGCCATCTTCCCCCACTGGC ACAGACTCTTGACCATCCAACTGGAAAGAGCTCTCGAGCACAATGGTGCACTGCTTGGTGTTCCTT ACTGGGACTGGACCAAGGACCTGTCGTCACTGCCGGCGTTCTTCTCCGACTCCAGCAACAACAATC CCTACTTCAAGTACCACATCGCAGGTGTTGGTCACGACACCGTCAGAGAGCCAACTAGTCTTATAT ATAACCAGCCCCAAATCCATGGTTATGATTATCTCTATTACCTAGCATTGACCACGCTTGAAGAAA ACAATTACTGTGACTTTGAGGTTCAGTATGAGATCCTCCACAACGCCGTCCACTCCTGGCTTGGAG GATCCCAGAAGTATTCCATGTCTACCCTGGAGTATTCGGCCTTTGACCCTGTCTTTATGATCCTTC ACTCGGGTCTAGACAGACTTTGGATCATCTGGCAAGAACTTCAGAAGATCAGGAGAAAGCCCTACA ACTTCGCTAAATGTGCTTATCATATGATGGAAGAGCCACTGGCGCCCTTCAGCTATCCATCTATCA ACCAGGACGAGTTCACCCGTGCCAACTCCAAGCCTTCTACAGTTTTTGACAGCCATAAGTTCGGCT ACCATTACGATAACCTGAATGTTAGAGGTCACAGCATCCAAGAACTCAACAATCATCAATGACT AGATCTATCTCCGAACAGATGACAATGACGAAGAAGTTGGAACTTTCACTGTCCTGGGAGGAGAGA GGGAAATGCCATGGGCCTACGAGCGAGTTTTCAAGTATGACATCACAGAGGTTGCAGATAGACTTA AACTAAGTTATGGGGACACCTTTAACTTCCGACTAGAGATCACATCCTACGATGGATCGGTGGTAA ACAAGAGCCTACCCAATCCTTTCATCATCTACAGACCTGCCAATCATGACTACGATGTTCTTGTTA TCCCAGTAGGAAGAAACCTTCACATCCCTCCCAAAGTTGTCGTCAAGAGAGGCACCCGCATCGAGT TCCACCCAGTCGATGATTCAGTTACGAGACCAGTTGTTGATCTTGGAAGCTACACTGCACTCTTCA ACTGTGTGGTACCACCGTTCACATACCGCGGATTCGAACTGAACCACGTCTATTCTGTCAAGCCTG GTGACTACTATGTTACCGGACCAACGAGAGACCTTTGCCAGAATGCAGATGTCAGGATTCATATCC ATGTTGAGGATGAGTAA

3'UTR

**CGCAACAG** 

INTRON 3'UTR (SEQ ID NO:138)

#### 3´UTR

# Figure 7

# Primary structure of the HtH2 protein

## DOMAIN A (SEQ ID NO:156)

GLPYWDWTQHLTQLPDLVSDPLFVDPEGGKAHDNAWYRGNIKFENKKTARAVDDRLFEKVGPGENT RLFEGILDALEQDEFCNFEIQFELAHNAIHYLVGGRHTYSMSHLEYTSYDPLFFLHHSNTDRIFAI WQRLQVLRGKDPNTADCAHNLIHEPMEPFRRDSNPLDLTRENSKPIDSFDYAHLGYQYDDLTLNGM TPEELNSYLHERSGKEGVFASFRLSGFGGSANVVVYACRPAHDEMAVDQCDKAGDFFVLGGPTEMP WRFYRAFHFDVTDSIDNIDKDRHGHYYVKAELFSVNGSALPNDLLPQPTISHRPARGHVDEAPAPS SDAHLAVRKDINHLTREEVYELRRAMERFQADTSVDGYQATVEYHGLPARCPFPEATNRFACCIHG MATFPHW

### DOMAIN B

HRLFVTQVEDALIRRGSPIGVPYWDWTQPMAHLPGLADNATYRDPISGDSRHNPFHDVEVAFENGR TERHPDSRLFEQPLFGKHTRLFDSIVYAFEQEDFCDFEVQFEMTHNNIHAWIGGGGKYSMSSLHYT AFDPISYLHHSNTDRLWAIWQALQIRRNKPYKAHCAWSEERQPLKPFAFSSPLNNNEKTYENSVPT NVYDYEGVLGYTYDDLNFGGMDLGQLEEYIQRQRQRDRTFAGFFLSHIGTSANVEIIIDHGTLHTS VGTFAVLGGEKEMKWGFDRLYKYEITDELRQLNLRADDGFSISVKVTDVDGSELSSELIPSAAIIF ERSH

## DOMAIN C

IDHQDPHQDTIIRKNVDNLTPEEINSLRRAMADLQSDKTAGGFQQIAAFHGEPKWCPSPDAEKKFS CCVHGMAVFPHWHRLLTVQGENALRKHGCLGALPYWDWTRPLSHLPDLVSQQNYTDAISTVEARNP WYSGHIDTVGVDTTRSVRQELYEAPGFGHYTGVAKQVLLALEQDDFCDFEVQFEIAHNFIHALVGG SEPYGMASLRYTTYDPIFYLHHSNTDRLWAIWQALQKYRGKPYNSANCAIASMRKPLQPFGLTDEI NPDDETRQHAVPFSVFDYKNNFNYEYDTLDFNGLSISQLDRELSRRKSHDRVFAGFLLHGIQQSAL VKFFVCKSDDDCDHYAGEFYILGDEAEMPWGYDRLYKYEITEQLNALDLHIGDRFFIRYEAFDLHG TSLGSNIFPKPSVIHDEGA

#### DOMAIN D

GHHQADEYDEVVTAASHIRKNLKDLSKGEVESLRSAFLQLQNDGVYENIAKFHGKPGLCDDNGRKV ACCVHGMPTFPQWHRLYVLQVENALLERGSAVSVPYWDWTETFTELPSLIAEATYFNSRQQTFDPN PFFRGKISFENAVTTRDPQPELYVNRYYYQNVMLAFEQDNYCDFEIQFEMVHNVLHAWLGGRATYS ISSLDYSAFDPVFFLHHANTDRLWAIWQELQRYRKKPYNEADCAINLMRKPLHPFDNSDLNHDPVT FKYSKPTDGFDYQNNFGYKYDNLEFNHFSIPRLEEIIRIRQRQDRVFAGFLLHNIGTSATVEIFVC VPTTSGEQNCENKAGTFAVLGGETEMAFHFDRLYRFDISETLRDLGIQLDSHDFDLSIKIQGVNGS YLDPHILPEPSLIFVPGSS

### DOMAIN E

SFLRPDGHSDDILVRKEVNSLTTRETASLIHALKSMQEDHSPDGFQAIASFHALPPLCPSPSATHR YACCVHGMATFPQWHRLYTVQFQDALRRHGAAVGVPYWDWLRPQSHLPELVTMETYHDIWSNRDFP NPFYQANIEFEGENITTEREVIADKLFVKGGHVFDNWFFKQAILALEQENYCDFEIQFEILHNGVH TWVGGSRTHSIGHLHYASYDPLFYLHHSQTDRIWAIWQELQEQRGLSGDEAHCALEQMREPLKPFS FGAPYNLNQLTQDFSRPEDTFDYRKFGYEYDNLEFLGMSVAELDQYIIEHQENDRVFAGFLLSGFG GSASVNFQVCRADSTCQDAGYFTVLGGSAEMAWAFDRLYKYDITETLEKMHLRYDDDFTISVSLTA NNGTVLSSSLIPTPSVIFQRGH

## DOMAIN F

RDINTKSMSANRVRRELSDLSARDPSSLKSALRDLQEDDGPNGYQALAAFHGLPAGCHDSQGNEIA CCIHGMPTFPQWHRLYTLQLEMALRRHGSSVAIPYWDWTKPISELPSLFTSPEYYDPWHDAVVNNP FSKGFVKFANTYTVRDPQEMLFQLCEHGESILYEQTLLALEQTDYCDFEVQFEVLHNVIHYLVGGR QTYALSSLHYASYDPFFFIHHSFVDKMWVVWQALQKRRKLPYKRADCAVNLMTKPMRPFDSDMNQN PFTKMHAVPNTLYDYETLYYSYDNLEIGGRNLDQLQAEIDRSRSHDRVFAGFLLRGIGTSADVRFW ICRNENDCHRGGIIFILGGAKEMPWSFDRNFKFDITHVLEKAGISPEDVFDAEEPFYIKVEIHAVN KTMIPSSVIPAPTIIYSPGE

#### DOMAIN G

GRAADSAHSANIAGSGVRKDVTTLTVSETENLRQALQGVIDDTGPNGYQAIASFHGSPPMCEMNGR KVACCAHGMASFPHWHRLYVKQMEDALADHGSHIGIPYWDWTTAFTELPALVTDSENNPFHEGRID HLGVTTSRSPRDMLFNDPEQGSESFFYRQVLLALEQTDYCQFEVQFELTHNAIHSWTGGRSPYGMS TLEFTAYDPLFWLHHSNTDRIWAVWQALQKYRGLPYNEAHCEIQVLKQPLRPFNDDINHNPITKTN ARPIDSFDYERFNYQYDTLSFHGKSIPELNDLLEERKREERTFAAFLLRGIGCSADVVFDICRPNG DCVFAGTFAVLGGELEMPWSFDRLFRYDITRVMNQLHLQYDSDFSFRVKLVATNGTELSSDLLKSPTIEHEL

### DOMAIN H

GAHRGPVEETEVTHQNTDGNAHFHRKEVDSLSLDEANNLKNALYKLQNDHSLTGYEAISGYHGYPN LCPEEGDDKYPCCVHGMAIFPHWHRLLTIQLERALEHNGALLGVPYWDWTKDLSSLPAFFSDSSNN NPYFKYHIAGVGHDTVREPTSLIYNQPQIHGYDYLYYLALTTLEENNYCDFEVQYEILHNAVHSWL GGSQKYSMSTLEYSAFDPVFMILHSGLDRLWIIWQELQKIRRKPYNFAKCAYHMMEEPLAPFSYPS INQDEFTRANSKPSTVFDSHKFGYHYDNLNVRGHSIQELNTIINDLRNTDRIYAGFVLSGIGTSAS VKIYLRTDDNDEEVGTFTVLGGEREMPWAYERVFKYDITEVADRLKLSYGDTFNFRLEITSYDGSV VNKSLPNPFIIYRPANHDYDVLVIPVGRNLHIPPKVVVKRGTRIEFHPVDDSVTRPVVDLGSYTAL FNCVVPPFTYRGFELNHVYSVKPGDYYVTGPTRDLCQNADVRIHIHVEDE

# Figure 8

# Genomic sequence of the KLH1 gene

#### DOMAIN 1B

GGCCTACCGTACTGGGACTGGACTGAACCCATGACACACATTCCGGGTCTGGCAGGAAACAAAACT
TATGTGGATTCTCATGGTGCATCCCACACAAATCCTTTTCATAGTTCAGTGATTGCATTTGAAGAA
AATGCTCCCCACACCAAAAGACAAATAGATCAAAGACTCTTTAAACCCGCTACCTTTGGACACCAC
ACAGACCTGTTCAACCAGATTTTGTATGCCTTTGAACAAGAAGATTACTGTGACTTTGAAGTCCAA
TTTGAGATTACCCATAACACGATTCACGCTTGGACAGGAGGAAGACATTTCTCAATGTCGTCC
CTACATTACACAGCTTTCGATCCTTTGTTTTACTTTCACCATTCTAACGTTGATCGTCTTTGGGCC
GTTTGGCAAGCCTTACAGATGAGACGGCATAAACCCTACAGGGCCCACTGCGCCATATCTCTGGAA
CATATGCATCTGAAACCATTCGCCTTTTCATCTCCCCTTAACAATAACGAAAAGACTCATGCCAAT
GCCATGCCAAACAAGATCTACGACTATGAAAATGTCCTCCATTACACATACGAAGATTTAACATTT
GGAGGCATCTCTCTGGGAAAACATAGAAAAGATGATCCACGAAAACCAGCAAGAAGACAGAATATAT
GCCGGTTTTCTCCTGGCTGGCATACGTACTTCAGCAAATGTTGATATCTTCATTAAAACTACCGAT
TCCGTGCAACATAAGGCTGGAACATTTGCAGTGCTCGGTGGAAGCAAGAAATGAAGTGGGGGATTT
GATCGCGTTTTCAAGTTTGACATCACGCACGTTTTGAAAGATCTCGATCTCACTGCTGATGGCGAT
TTCGAAGTTACTGTTGACATCACTGAAGTCGATGGAACTTAAACTTTCCACAT
GCTTCTGTCATTCGTGAGCATGCACGTGGTAAGCTGAATAGAG

INTRON 1B/1C(SEQ ID NO:139)

### DOMAIN 1C

INTRON 1C/1D (SEQ ID NO:140)

#### DOMAIN 1D

GTCACCATGAAGGCGAAGTATATCAAGCTGAAGTAACTTCTGCCAACCGTATTCGAAAAAACATTG AAAATCTGAGCCTTGGTGAACTCGAAAGTCTGAGAGCTGCCTTCCTGGAAAATTGAAAACGATGGAA CTTACGAATCAATAGCTAAATTCCATGGTAGCCCTGGTTTGTGCCAGTTAAATGGTAACCCCATCT CTTGTTGTCCATGCCATGCCAACTTTCCCTCACTGGCACAGACTGTACGTGGTTGTCGTTGAGA ATGCCCTCCTGAAAAAAGGATCATCTGTAGCTGTTCCCTATTGGGACTGGACAAAACGAATCGAAC ATTTACCTCACCTGATTTCAGACGCCACTTACTACAATTCCAGGCAACATCACTATGAGACAAACC CATTCCATCATGGCAAAATCACACGAGAATGAAATCACTACTAGGGATCCCAAGGACAGCCTCT TCCATTCAGACTACTTTTACGAGCAGGTCCTTTACGCCTTGGAGCAGGATAACTTCTGTGATTTCG AGATTCAGTTGGAGATATTACACAATGCATTGCATTCTTTACTTGGTGGCAAAGGTAAATATTCCA TCTGGGCAATCTGGCAAGACCTTCAGAGGTTCCGAAAACGGCCATACCGAGAAGCGAATTGCGCTA TCCAATTGATGCACACGCCACTCCAGCCGTTTGATAAGAGCGACAACAATGACGAGGCAACGAAAA CGCATGCCACTCCACATGATGGTTTTGAATATCAAAACAGCTTTGGTTATGCTTACGATAATCTGG TATTCGCTGGCTTCCTCCTTCACAATATTGGAACATCTGCCGATGGCCATGTATTTGTATGTCTCC CAACTGGGGAACACGAAGGACTGCAGTCATGAGGCTGGTATGTTCTCCATCTTAGGCGGTCAAA CGGAGATGTCCTTTGTATTTGACAGACTTTACAAACTTGACATAACTAAAGCCTTGAAAAAGAACG GTGTGCACCTGCAAGGGGATTTCGATCTGGAAATTGAGATTACGGCTGTGAATGGATCTCATCTAG ACAGTCATGTCATCCACTCTCCCACTATACTGTTTGAGGCCGGAACAG

INTRON 1D/1E (SEQ ID NO:141)

#### DOMAIN 1E

INTRON 1E/1F (SEQ ID NO:142)

DOMAIN 1F-1 (1st part of domain f)

INTRON 1F-1/1F-2 (SEQ ID NO:143)

DOMAIN 1F-2 (2nd part of domain f)

INTRON 1F-2/1G-1 (SEO ID NO:144)

DOMAIN 1G-1 (1st part of domain g)

ACCATCACGAAGATCATCATTCTTCTTCTATGGCTGGACATGGTGTCAGAAAGGAAATCAACACAC TTACCACTGCAGAGGTGGACAATCTCAAAGATGCCATGAGAGCCGTCATGGCAGACCACCGTCCAA ATGGATACCAGGCTATAGCAGCGTTCCATGGAAACCCACCAATGTGCCCTATGCCAGATGGAAAGA ATTACTCGTGTTGTACACATG

INTRON G1-1/1G-2 (SEQ ID NO:145)

GTATGTATTTCCCACTGGTGGTCGCTGACTGCCAACACATACTTGTAATTTATTCATGAAAGTATA ATAGTTTGTTTGAAAGTATATTTATAACCATCTTGCACAAGCGTCACGAATTTTCACCACAAAGCT TCAAAACGCCCAAAACATTCTAATAGCGATATATTTGTTAAAAGACCAAAATATAGCCTTACAACA TATGTACTAACTGCCAATCTCATAATACTTGCCTTGGATGTGCTTCTTTTTCACATTCGCGTCGAG TCCCTCCAGGCCAGGCTTTATTTGTCTCTTATAGAATATATCGCTATTAGAATGTTTTTGACGTTT ATCTTTTCAAACAAGATTTTAGTATTTTGAAGACTTCTATGAATAAATTACACTTATGTGTTAGGT ATAGTTATCCTACTGTGGATAGTCTATATGAGAATCGTTGAAAGAATAATACAATTCTAATGGATT GCAACTTCTTTAACTTTTATTTGCAACTGCCACGTTTCGGTATACGTTCTTATGCCGTCATCAAGC ATACGAGTGTACATGTATGCCAAAACGCTGCAAATAAAAATTAAAGAAGTTGCAATCCATAAGAAT TTCAATGTTCTTTCATCATCACATCAACTTCTAAAAATGCCTATAAAACAATCAACAAACGTACAA TAGTACATTACCGGATCTCGCAGCATGACCACGTCGATATCTAAACAATATCACTATCCATTAATA GGATCAAGAGTAGGTACAGACATGTTCAGTTATAAATACTCTTCAAAAAAGTAGGGGAACTTGGAA TTTCAAGGTCAATAACAAACTAATGATAATAACAATTGGTCCCAAATAATAACAATTGGTCCCAAA CTAATTGTATCTTTACAAAGAAGAAATTGAGTGAACAATTCACCCGGTATTTTATTACCTAAACCG

DOMAIN 1G-2 (2nd part of domain g)

GCATGGCTACTTTCCCCCACTGGCACAGACTGTACACAAAACAGATGGAAGATGCCTTGACCGCCC ATGGTGCCAGAGTCGGCCTTCCTTACTGGGACGGACAACTGCCTTTACAGCTTTGCCAACTTTTG TCACAGATGAAGAGGACAATCCTTTCCATCAT

INTRON 1G-2/1G-3 (SEQ ID NO:146)

GTGAGTTCACGTAAGCCTACGAGATCAACATTACTCCTTAACAGCCACGGCATCATGTACCGATATAAGGACATGAGTCTGAAATAAACATGACTTGACACCGTTGTGGTCACAGTTTTGTTTCTCATTGGTGAACCTGTGAAACAACCTTTCAAACCAAAAGATGCCTATTAATATTGTTAATTCCCATGAATTAGG AGATACACACATTCTACTGTCATTT.....AATAACCGCTTC CAGCATGAAAACACAATATGATTATCTCAATTCTACCATTACTAATTATAATTTTTGACTGGCATTATTTGACGACGCGTAAAACATCGCTGCTTTACAGACTGCACTGCGGTAACTGTGACGTTTTCATGACGTCACTACATTCTATTCAAAACATTTCCACAGAAGAGCGAGACCACGGCCGTGATGGGTTCTGGGCAGATGATTACCCAAGTATATATTTATAATAACTTGACTGCTTGCCTGAATAATGTTGACACATGACAACGAATTTGTGATAGCGTAAGAGCGTGAATACTGTGAATAGTGTGAGGGGTGTTTGCTGAGAGTTAACCACCGTTAATTGCAAAATTCCCGAATACTTGCATTTGCAGTCGAAGAAGAATTGCATTCTTACTCCTGTGAATGGACTCATTGTTATTTAGCAGCGGTTATTGAGGTTTTTGATCACCTCTAAATAGAC*AATCAGGATGCGGCAAACCGGAAAATTATAGCAGAATCTGTAATTCAAGATGGGCTTGCCTGTGAA* AATATGCTGCGAGTTCAGTAACACTTTTCCCTTTCGATCATGGCCTGTTTTGCTCTGAATCTGGTC

DOMAIN 1G-3 (3rd part of domain g)

# Figure 9

# Primary structure of the KLH1 protein

#### DOMAIN B

GLPYWDWTEPMTHIPGLAGNKTYVDSHGASHTNPFHSSVIAFEENAPHTKRQIDQRLFKPATFGHH TDLFNQILYAFEQEDYCDFEVQFEITHNTIHAWTGGSEHFSMSSLHYTAFDPLFYFHHSNVDRLWA VWQALQMRRHKPYRAHCAISLEHMHLKPFAFSSPLNNNEKTHANAMPNKIYDYENVLHYTYEDLTF GGISLENIEKMIHENQQEDRIYAGFLLAGIRTSANVDIFIKTTDSVQHKAGTFAVLGGSKEMKWGF DRVFKFDITHVLKDLDLTADGDFEVTVDITEVDGTKLASSLIPHASVIREHARGKLNR

### DOMAIN C

VKFDKVPRSRLIRKNVDRLSPEEMNELRKALALLKEDKSAGGFQQLGAFHGEPKWCPSPEASKKFA CCVHGMSVFPHWHRLLTVQSENALRRHGYDGALPYWDWTSPLNHLPELADHEKYVDPEDGVEKHNP WFDGHIDTVDKTTTRSVQNKLFEQPEFGHYTSIAKQVLLALEQDNFCDFEIQYEIAHNYIHALVGG AQPYGMASLRYTAFDPLFYLHHSNTDRIWAIWQALQKYRGKPYNVANCAVTSMREPLQPFGLSANI NTDHVTKEHSVPFNVFDYKTNFNYEYDTLEFNGLSISQLNKKLEAIKSQDRFFAGFLLSGFKKSSL VKFNICTDSSNCHPAGEFYLLGDENEMPWAYDRVFKYDITEKLHDLKLHAEDHFYIDYEVFDLKPA SLGKDLFKQPSVIHEPRI

## DOMAIN D

GHHEGEVYQAEVTSANRIRKNIENLSLGELESLRAAFLEIENDGTYESIAKFHGSPGLCQLNGNPI SCCVHGMPTFPHWHRLYVVVVENALLKKGSSVAVPYWDWTKRIEHLPHLISDATYYNSRQHHYETN PFHHGKITHENEITTRDPKDSLFHSDYFYEQVLYALEQDNFCDFEIQLEILHNALHSLLGGKGKYS MSNLDYAAFDPVFFLHHATTDRIWAIWQDLQRFRKRPYREANCAIQLMHTPLQPFDKSDNNDEATK THATPHDGFEYQNSFGYAYDNLELNHYSIPQLDHMLQERKRHDRVFAGFLLHNIGTSADGHVFVCL PTGEHTKDCSHEAGMFSILGGQTEMSFVFDRLYKLDITKALKKNGVHLQGDFDLEIEITAVNGSHL DSHVIHSPTILFEAG

## DOMAIN E

TDSAHTDDGHTEPVMIRKDITQLDKRQQLSLVKALESMKADHSSDGFQAIASFHALPPLCPSPAAS KRFACCVHGMATFPQWHRLYTVQFQDSLRKHGAVVGLPYWDWTLPRSELPELLTVSTIHDPETGRD IPNPFIGSKIEFEGENVHTKRDINRDRLFQGSTKTHHNWFIEQALLALEQTNYCDFEVQFEIMHNG VHTWVGGKEPYGIGHLHYASYDPLFYIHHSQTDRIWAIWQSLQRFRGLSGSEANCAVNLMKTPLKP FSFGAPYNLNDHTHDFSKPEDTFDYQKFGYIYDTLEFAGWSIRGIDHIVRNRQEHSRVFAGFLLEG FGTSATVDFQVCRTAGDCEDAGYFTVLGGEKEMPWAFDRLYKYDITETLDKMNLRHDEIFQIEVTITSYDGTVLDSGLIPTPSIIYDPAH

#### DOMAIN F

HDISSHHLSLNKVRHDLSTLSERDIGSLKYALSSLQADTSADGFAAIASFHGLPAKCNDSHNNEVA CCIHGMPTFPHWHRLYTLQFEQALRRHGSSVAVPYWDWTKPIHNIPHLFTDKEYYDVWRNKVMPNP FARGYVPSHDTYTVRDVQEGLFHLTSTGEHSALLNQALLALEQHDYCDFAVQFEVMHNTIHYLVGG PQVYSLSSLHYASYDPIFFIHHSFVDKVWAVWQALQEKRGLPSDRADCAVSLMTQNMRPFHYEINH NQFTKKHAVPNDVFKYELLGYRYDNLEIGGMNLHEIEKEIKDKQHHVRVFAGFLLHGIRTSADVQF QICKTSEDCHHGGQIFVLGGTKEMAWAYNRLFKYDITHALHDAHITPEDVFHPSEPFFIKVSVTAV NGTVLPASILHAPTIIYEPGLG

# 37 / 44

# DOMAIN G

 $\label{thm:condition} D H H E D H H S S MAGHGVRKE INTLTTAE V D N L K D AMRAVMA D H G P N G Y QA I AAF H G N P P M C P M P D G K N Y S C C T H G M A T F P H W H R L Y T K Q M E D A L T A H G A R V G L P Y W D G T T A F T A L P T F V T D E E D N P F H H G H I D Y L G V D T T R S P R D K L F N D P E R G S E S F F Y R Q V L L A L E Q T D \\$ 

#### 38 / 44

# Figure 10

# Genomic sequence of the KLH2 gene

#### DOMAIN 2B

INTRON 2B/2C (SEQ ID NO:147)

GTATTTAAAAAGTAATAAAACCATATTTTCGAATGCGCTTTATGAAATATCGTGTGACTGGTTCT TTAGTTTACATGGAGTGTAACAACATGCTCCATCAGTTGACATATACTGCTCACACAAAGTAAGGG ATATTTGATAATGATAACAAATATAATCAAAGCGGTTATACTATCAAGACTTATTCACATAATTAC AGGTGAAGGGAGGTGTGATCGTGTTCACTGATCAGGTTGAGGCCAGAGAAGTCCCAGTTTGAGTCT TGCAGAAGATGATGTTTAGGCATGGGGTCGAATCACCAAAATCACATGACTTCAATAACGGGTTGG ACCACCTCGAGCGACGATGCAAGCAGTAGAGCGTCTACGCATGCTCCTGATAAGGCGACCAATCTG TTCCTGGGGAATCAGTCGCCACTCCTCTTGTAGTGCCACGCTCATTTCTGCTACGGTCCTGGGTAC CTGCTATCGGGTCTTGATCCGTATCCCAAGGATGTCCCACACATGTTCAAGGTGAGAGGTCGGGGA ACATCGCTGGCCACGGTAAGGTCTGAATTTGATGCCGTTGAAAGTGAGCTCTGACAACCTGAGCAT GGTGAGCTCTGACGTTGTCGTCCTGAAAGATGAATCCAGCTCCATGACAGCGAGCAAAGGGCAGGA CGTGTTGGTCAATGCAGTTGTCTCTGCAGTACACCCTGTCACTCGCCACTCACAAGCGTGTAGAT CTGTACGACCAGTCATGGAGATCCCAGCCCACATCATAACGGACCCCTATCCATACCGATCATGAG CCACCATAGCAGCGTCTTGATGACGTTCTCCCTGTCGCCTCGACATCCTCACACGGCCAAAAGGAA CGTGGACTCGTCACTGAACATGACATTAGCCAACCTGGCACTTGTCCACCGCTGATGTTGGCGAGA CCATTCCAGTCGAGCTCTTCGGTGTCTGGCTTTCATCGATAACACGACGTAAGGTCTGCGGGCGTG CAAGACGGCTCTATGCAGGCGATTTCGGATTGTCTGGGTGCTAACTCTGATCCCAGGTGCCTGCTG AAGTTGATGCTGGATCTGTGGCATTGAGATGGCGATTCCTTAGGACTGTGGAGATGATGAATCG ATCTTGACTTATGGTGGTGACATTAGGACGTCGGGTTCGTGTCCTATCCTGCACTCTTCCAGTTGT TCGGTGACGCTCTGGTACCCGGCTGATTACTGACTGAGAATATCCATCTGCCGTGCGACATGAGCC TGTGTTGGCCCAGCCTGAAGCATTGCAATCGCCAGAGACGCTCTTCAAAAGTCATTCGACGCATGG TTTTCTGTTCACAAATGACAGCGTAAAACAGTTTTTGGTGCTTTTATGCTTCCCAAGAGCATGAAA AACACGTTCTATGGGTCGTGCACACCTTACATGACAAGTGTGAAAAGTGACTTGCACCCCCTTGTG TGTTCGGATGCACACTCTGTTTACGTACTGATGCGATTTGGCGTCTAAACATGTTTTGGCGTCTAA ACATGTTTTCCTGCATGATTCATATACTATTTTGTCATATTCCTGGCATCAAACCAAACTACAGTG AAATATATTTCAATATCCCCTACTTTGTGTGAGTAGTATAGATCACTGCAGACAACATATAGACAA TGCAGTTACACCGTCAACAATCCCAGTCATTAATTATGATGACACTTCCACACATAGTGTCAGTGA TTGTAATTCAACTGTACACACTTTTCCCGTGAACATTCAGGATCTATATGACTAAATATATAACAT TAGTATACGTGCAGTTTTGTATCGCTACGACATTGTTGTAACTCTTTGTTTAATCATTTAACAG

#### DOMAIN 2C

CTGATGCCAAAGACTTTGGCCATAGCAGAAAAATCAGGAAAGCCGTTGATTCTCTGACAGTCGAAG AACAAACTTCGTTGAGGCGAGCTATGGCAGATCTACAGGACGACAAAACATCAGGGGGTTTCCAGC AGATTGCAGCATTCCACGGAGAACCAAAATGGTGTCCAAGCCCCGAAGCGGAGAAAAAATTTGCAT GCTGTGTTCATGGAATGGCTGTTTTCCCTCACTGGCACAGATTGCTGACAGTTCAAGGAGAAAATG CTCTGAGGAAACATGGATTTACTGGTGGATTGCCCTATTGGGACTGGACTCGGCCAATGAGCGCCC TTCCACATTTTGTTGCTGATCCTACTTACAATGATTCTGTTTCCAGCCTCGAAGAAGATAACCCAT GGTATCATGGTCACATAGATTCTGTTGGGCATGATACTACAAGAGCTGTGCGTGATGATCTTTATC AATCTCCTGGTTTCGGTCACTACACAGATATTGCAAAACAAGTCCTTCTGGCCTTTGAGCAGGACG ACGAACCATACAGTATGTCATCTTTGAGGTATACTACATACGATCCAATCTTCTTCTTGCACCGCT CCAATACAGACCGACTTTGGGCCATTTGGCAAGCTTTGCAAAAATACCGGGGGAAACCATACAACA CTGCAAACTGTGCCATTGCATCCATGAGAAAACCACTTCAGCCATTTGGTCTTGATAGTGTCATAA ATCCAGATGACGAAACTCGTGAACATTCGGTTCCTTTCCGAGTCTTCGACTACAAGAACAACTTCG ACTATGAGTATGAGAGCCTGGCATTTAATGGTCTGTCTATTGCCCAACTGGACCGAGAGTTGCAGA GAAGAAAGTCACATGACAGAGTCTTTGCAGGATTCCTTCTTCATGAAATTGGACAGTCTGCACTCG TGAAATTCTACGTTTGCAAACACAATGTATCTGACTGTGACCATTATGCTGGAGAATTCTACATTT TGGGAGATGAAGCTGAGATGCCTTGGAGGTATGACCGTGTGTACAAGTACGAGATAACACAGCAGC TGCACGATTTAGATCTACATGTTGGAGATAATTTCTTCCTTAAATATGAAGCCTTTGATCTGAATG GCGGAAGTCTTGGTGGAAGTATCTTTTCTCAGCCTTCGGTGATTTTCGAGCCAGCTGCAG

INTRON 2C/2D (SEQ ID NO:148)

#### DOMAIN 2D

GTTCACACCAGGCTGATGAATATCGTGAGGCAGTAACAAGCGCTAGCCACATAAGAAAAATATCC GGGACCTCTCAGAGGGAGAAATTGAGAGCATCAGATCTGCTTTCCTCCAAATTCAAAAAGAGGGTA TATATGAAAACATTGCAAAGTTCCATGGAAAACCAGGACTTTGTGAACATGATGGACATCCTGTTG CTTGTTGTGTCCATGGCATGCCCACCTTTCCCCACTGGCACAGACTGTACGTTCTTCAGGTGGAGA ATGCGCTCTTAGAACGAGGGTCTGCAGTTGCTGTTCCTTACTGGGACTGGACCGAGAAAGCTGACT CTCTGCCATCATTAATCAATGATGCAACTTATTTCAATTCACGATCCCAGACCTTTGATCCTAATC CTTTCTTCAGGGGACATATTGCCTTCGAGAATGCTGTGACGTCCAGAGATCCTCAGCCAGAACTAT GGGACAATAAGGACTTCTACGAGAATGTCATGCTGGCTCTTGAGCAAGACAACTTCTGTGACTTTG AGATTCAGCTTGAGCTGATACACAACGCCCTTCATTCTAGACTTGGAGGAAGGGCTAAATACTCCC TTTCGTCTCTTGATTATACCGCATTTGATCCTGTATTTTTCCTTCACCATGCAAACGTTGACAGAA TCAACGAGATGCGTAAACCTCTTCAACCATTTAATAACCCAGAACTTAACAGTGATTCCATGACGC TTAAACACAACCTCCCACAAGACAGTTTTGATTATCAAAACCGCTTCAGGTACCAATATGATAACC TTCAATTTAACCACTTCAGCATACAAAAGCTAGACCAAACTATTCAGGCTAGAAAACAACACGACA GAGTTTTTGCTGGCTTTATTCTTCACAACATTGGGACATCTGCTGTTGTAGATATTTATATTTGCG TTGAACAAGGAGGAGAACAAAACTGCAAGACAAAGGCGGGTTCCTTCACGATTCTGGGGGGGAGAA CAGAAATGCCATTCCACTTTGACCGCTTGTACAAATTTGACATAACGTCTGCTCTGCATAAACTTG GTGTTCCCTTGGACGGACATGGATTCGACATCAAAGTTGACGTCAGAGCTGTCAATGGATCGCATC ATG

### 40 / 44

INTRON 2D/2E (SEQ ID NO:149)

GTTATAAAGCAGTATATTCTCTTCAAAAAAGTAGGGGAACTTGGAATTTCAAGGTAAATAACATAA
CTACCTTCAACGGCACAATATCCATATGATGCCCTGGCCAGCAATGAGGCCTGATCTTTTCCCCAT
TAAAAATGTCTGGAACATCTTGGGCAAACGTGTGCGTCAACGTAAAACGCCACCAGTCACGCTAGA
TGAACTTGTCCAGGCGTTGGTGGAAGAATGGGACAGACTGCATCAATTACCATAAGTAGACTCATT
TGCAGCGAATCAGTCAGTGTTTGACCAATAACGGGGGCATTACGCACTACTGACGCAAAACAATGT
CAATTTCCGTTTCTTACCCATTCCTTTCTTCACGGACCATAACAGCAAGAGAAACTGNTTAGGTAA
TGAAATACCGGTGAATTATTGTTAACTGGATTCCTTCTTTGTAAAGATACAATTAGTTTGGGACCA
ATTATTATTATCATTAGTTTGTTAATTGACCTTGAAATTCGAAGTTCCTCTACATTTTTTAAGGAGT
TTATTTGATTGACAATGAAATGTAAGAAAAGAGCAAATCGTAAAAATACGTTAAAAATTATTCCTTA
AACATCAGTCTCTAACTTCAGTTTAAATTGCCAGTAACACGTGTTATATGATGTTCCGTTTCTCT
TTGTTTTTTAGCATTCAACTTCATTTTGATATAACGTTTTACTGTTTTTAGATTCACATCAAACTGCAG

#### DOMAIN 2E

ATGGGCTTTCACAACATAATCTTGTGCGAAAAGAAGTAAGCTCTCTTACAACACTGGAGAAACATT TTTTGAGGAAAGCTCTCAAGAACATGCAAGCAGATGATTCTCCAGACGGATATCAAGCTATTGCTT  $\tt CTTTCCACGCTTTGCCTCTTTTGTCCAAGTCCATCTGCTGCACATAGACACGCTTGTTGCCTCC$ ATGGTATGGCTACCTTCCCTCAGTGGCACAGACTCTACACAGTTCAGTTCGAAGATTCTTTGAAAC GACATGGTTCTATTGTCGGACTTCCATATTGGGATTGGCTGAAACCGCAGTCTGCACTCCCTGATT TGGTGACACAGGAGACATACGAGCACCTGTTTTCACACAAAACCTTCCCAAATCCGTTCCTCAAGG CAAATATAGAATTTGAGGGAGAGGGAGTAACAACAGAGAGGGATGTTGATGCTGAACACCTCTTTG CAAAAGGAAATCTGGTTTACAACAACTGGTTTTGCAATCAGGCACTATATGCACTAGAACAAGAAA CAAAGACCCATTCAATAGGTCATCTTCATTACGCATCATACGATCCACTGTTCTATATCCACCATT CGCAGACAGATCGCATTTGGGCTATCTGGCAAGCTCTCCAGGAGCACAGAGGTCTTTCAGGGAAGG AAGCACACTGCGCCCTGGAGCAAATGAAAGACCCTCTCAAACCTTTCAGCTTTGGAAGTCCCTATA ATTTGAACAACGCACTCAAGAGTTCTCCAAGCCTGAAGACACATTTGATTATCACCGATTCGGGT ATGAGTATGATTCCCTCGAATTTGTTGGCATGTCTGTTTCAAGTTTACATAACTATATAAAACAAC AACAGGAAGCTGATAGAGTCTTCGCAGGATTCCTTCTTAAAGGATTTGGACAATCAGCATCCGTAT CGTTTGATATCTGCAGACCAGACCAGAGTTGCCAAGAAGCTGGATACTTCTCAGTTCTCGGTGGAA GTTCAGAAATGCCGTGGCAGTTTGACAGGCTTTACAAGTACGACATTACAAAAACGTTGAAAGACA TGAAACTGCGATACGATGACACATTTACCATCAAGGTTCACATAAAGGATATAGCTGGAGCTGAGT TGGACAGCGATCTGATTCCAACTCCTTCTGTTCTCCTTGAAGAAGGAAAGC

INTRON 2E/2F (SEQ ID NO:150)

DOMAIN 2F-1 (1st part of domain f)

ATGGGATCAATGTACGTCACGTTGGTCGTAATCGGATTCGTATGGAACTATCTGAACTCACCGAGA GAGATCTCGCCAGCCTGAAATCTGCAATGAGGTCTCTACAAGCTGACGATGGGGTGAACGGTTATC AAGCCATTGCATCATTCCACGGTCTCCCGGCTTCTTGTCATGATGATGAGGGACATGAG INTRON 2F (SEQ ID NO:151)

DOMAIN 2F-2 (2nd part of domain f)

ATTGCCTGTTGTATCCACGGAATGCCAGTATTCCCACACTGGCACAGGCTTTACACCCTGCAAATG GACATGGCTCTGTTATCTCACGGATCTGCTGTTGCTATTCCATACTGGGACTGGACCAAACCTATC AGCAAACTGCCTGATCTCTTCACCAGCCCTGAATATTACGATCCTTGGAGGGATGCAGTTGTCAAT AATCCATTTGCTAAAGGCTACATTAAATCCGAGGACGCTTACACGGTTAGGGATCCTCAGGACATT TTGTACCACTTGCAGGACGAAACGGGAACATCTGTTTTGTTAGATCAAACTCTTTTAGCCTTAGAG CAGACAGATTTCTGTGATTTTGAGGTTCAATTTGAGGTCGTCCATAATGCTATTCACTACTTGGTG GGTGGTCGACAAGTTTATGCTCTTTCTTCAACACTATGCTTCATATGACCCAGCCTTCTTTATT CATCACTCCTTTGTTGACAAAATATGGGCAGTCTGGCAAGCTCTGCAAAAGAAGAGAAAAGCGTCCC TATCATAAAGCGGATTGTGCTCTTAACATGATGACCAAACCAATGCGACCATTTGCACACGATTTC AATCACAATGGATTCACAAAAATGCACGCAGTCCCCAACACTCTATTTGACTTTCAGGACCTTTTC TACACGTATGACAACTTAGAAATTGCTGGCATGAATGTTAATCAGTTGGAAGCGGAAATCAACCGG CGAAAAAGCCAAACAAGAGTCTTTGCCGGGTTCCTTCTACATGGCATTGGAAGATCAGCTGATGTA CGATTTTGGATTTGCAAGACAGCTGACGACTGCCACGCATCTGGCATGATCTTTATCTTAGGAGGT TCTAAAGAGATGCACTGGGCCTATGACAGGAACTTTAAATACGACATCACCCAAGCTTTGAAGGCT CAGTCCATACACCCTGAAGATGTTTTGACACTGATGCTCCTTTCTTCATTAAAGTGGAGGTCCAT GGTGTAAACAAGACTGCTCTCCCATCTTCAGCTATCCCAGCACCTACTATAATCTACTCAGCTGGT GAAG

INTRON 2F-2/2G (SEQ ID NO:152)

DOMAIN 2G-1 (1st part of domain g)

INTRON 2G-1/2G-2 (SEQ ID NO:153)

DOMAIN 2G-2 (2nd part of domain g)

GAATGGCATCTTTCCCTCACTGGCACAGACTGTTTGTGAAACAGATGGAGGATGCACTGGCTGCCCAGATGGAGCTCACATTGGCATACCATACTGGGATTGGACAAGTGCGTTTAGTCATCTGCCTAGACTGACCACGAGCACAATCCCTTCCACCAC

INTRON 2G-2/2G-3 (SEQ ID NO:154)

DOMAIN 2G-3 (3rd part of domain g)

INTRON 2G/2H (SEQ ID NO:155)

GTATGTTTTGAGATCCACATAATCTTCTACCCTGTCTCATTTCTAATGCTCTTCAATACACAATTT
ATATAGCCTTTGAGCTTCAGATGTATTACGGACAGGCATTACAGTATACATGTAATATGGTTTTCT
GCTATTTGCAAAAATTGTGTCCTATCTCTGTTCAGATCATCATGGCGGTGACACCTAG

DOMAIN 2H (SEO ID NO:159)

# Figure 11

# Primary structure of the KLH2 protein

#### DOMAIN B

GLPYWDWTMPMSHLPELATSETYLDPVTGETKNNPFHHAQVAFENGVTSRNPDAKLFMKPTYGDHT YLFDSMIYAFEQEDFCDFEVQYELTHNAIHAWVGGSEKYSMSSLHYTAFDPIFYLHHSNVDRLWAI WQALQIRRGKSYKAHCASSQEREPLKPFAFSSPLNNNEKTYHNSVPTNVYDYVGVLHYRYDDLQFG GMTMSELEEYIHKQTQHDRTFAGFFLSYIGTSASVDIFINREGHDKYKVGSFVVLGGSKEMKWGFD RMYKYEITEALKTLNVAVDDGFSITVEITDVDGSPPSADLIPPPAIIFDVVR

#### DOMAIN C

ADAKDFGHSRKIRKAVDSLTVEEQTSLRRAMADLQDDKTSGGFQQIAAFHGEPKWCPSPEAEKKFA CCVHGMAVFPHWHRLLTVQGENALRKHGFTGGLPYWDWTRPMSALPHFVADPTYNDSVSSLEEDNP WYHGHIDSVGHDTTRAVRDDLYQSPGFGHYTDIAKQVLLAFEQDDFCDFEVQFEIAHNFIHALVGG NEPYSMSSLRYTTYDPIFFLHRSNTDRLWAIWQALQKYRGKPYNTANCAIASMRKPLQPFGLDSVI NPDDETREHSVPFRVFDYKNNFDYEYESLAFNGLSIAQLDRELQRRKSHDRVFAGFLLHEIGQSAL VKFYVCKHNVSDCDHYAGEFYILGDEAEMPWRYDRVYKYEITQQLHDLDLHVGDNFFLKYEAFDLN GGSLGGSIFSQPSVIFEPAA

#### DOMAIN\_D

GSHQADEYREAVTSASHIRKNIRDLSEGEIESIRSAFLQIQKEGIYENIAKFHGKPGLCEHDGHPV ACCVHGMPTFPHWHRLYVLQVENALLERGSAVAVPYWDWTEKADSLPSLINDATYFNSRSQTFDPN PFFRGHIAFENAVTSRDPQPELWDNKDFYENVMLALEQDNFCDFEIQLELIHNALHSRLGGRAKYS LSSLDYTAFDPVFFLHHANVDRIWAIWQDLQRYRKKPYNEADCAVNEMRKPLQPFNNPELNSDSMT LKHNLPQDSFDYQNRFRYQYDNLQFNHFSIQKLDQTIQARKQHDRVFAGFILHNIGTSAVVDIYIC VEQGGEQNCKTKAGSFTILGGETEMPFHFDRLYKFDITSALHKLGVPLDGHGFDIKVDVRAVNGSH LDQHILNEPSLLFVPGERKNIYY

#### DOMAIN E

DGLSQHNLVRKEVSSLTTLEKHFLRKALKNMQADDSPDGYQAIASFHALPPLCPSPSAAHRHACCL HGMATFPQWHRLYTVQFEDSLKRHGSIVGLPYWDWLKPQSALPDLVTQETYEHLFSHKTFPNPFLK ANIEFEGEGVTTERDVDAEHLFAKGNLVYNNWFCNQALYALEQENYCDFEIQFEILHNGIHSWVGG SKTHSIGHLHYASYDPLFYIHHSQTDRIWAIWQALQEHRGLSGKEAHCALEQMKDPLKPFSFGSPY NLNKRTQEFSKPEDTFDYHRFGYEYDSLEFVGMSVSSLHNYIKQQQEADRVFAGFLLKGFGQSASV SFDICRPDQSCQEAGYFSVLGGSSEMPWQFDRLYKYDITKTLKDMKLRYDDTFTIKVHIKDIAGAE LDSDLIPTPSVLLEEGK

## DOMAIN F

HGINVRHVGRNRIRMELSELTERDLASLKSAMRSLQADDGVNGYQAIASFHGLPASCHDDEGHEIA CCIHGMPVFPHWHRLYTLQMDMALLSHGSAVAIPYWDWTKPISKLPDLFTSPEYYDPWRDAVVNNP FAKGYIKSEDAYTVRDPQDILYHLQDETGTSVLLDQTLLALEQTDFCDFEVQFEVVHNAIHYLVGG RQVYALSSQHYASYDPAFFIHHSFVDKIWAVWQALQKKRKRPYHKADCALNMMTKPMRPFAHDFNH NGFTKMHAVPNTLFDFQDLFYTYDNLEIAGMNVNQLEAEINRRKSQTRVFAGFLLHGIGRSADVRF WICKTADDCHASGMIFILGGSKEMHWAYDRNFKYDITQALKAQSIHPEDVFDTDAPFFIKVEVHGV NKTALPSSAIPAPTIIYSAGE

#### DOMAIN G

DHIAGSGVRKDVTSLTASEIENLRHALQSVMDDDGPNGFQAIAAYHGSPPMCHMPDGRDVACCTHG MASFPHWHRLFVKQMEDALAAHGAHIGIPYWDWTSAFSHLPALVTDHEHNPFHHGHIAHRNVDTSR SPRDMLFNDPEHGSESFFYRQVLLALEQTDFCQFEVQFEITHNAIHSWTGGHTPYGMSSLEYTAYD PLFYLHHSNTDRIWAIWQALQKYRGFQYNAAHCDIQVLKQPLKPFSESRNPNPVTRANSRAVDSFD

# 44 / 44

YERLNYQYDTLTFHGHSISELDAMLQERKKEERTFAAFLLHGFGASADVSFDVCTPDGHCAFAGTF AVLGGELEMPWSFERLFRYDITKVLKQMNLHYDSEFHFELKIVGTDGTELPSDRIKSPTIEHHGG

DOMAIN H (SEQ ID NO:158)

GHDHSERHDGFFRKEVGSLSLDEANDLKNALYKLQNDQGPNGYESIAGYHGYPFLCPEHGEDQYAC CVHGMPVFPHWHRLHTIQFERALKEHGSHLGLPYWDW